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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2	Dec 17	The CA Lexicon available in the CAPLUS and CA files
NEWS 3	Feb 06	Engineering Information Encompass files have new names
NEWS 4	Feb 16	TOXLINE no longer being updated
NEWS 5	Apr 23	Search Derwent WPINDEX by chemical structure
NEWS 6	Apr 23	PRE-1967 REFERENCES NOW SEARCHABLE IN CAPLUS AND CA
NEWS 7	May 07	DGENE Reload
NEWS 8	Jun 20	Published patent applications (A1) are now in USPATFULL
NEWS 9	JUL 13	New SDI alert frequency now available in Derwent's DWPI and DPCI
NEWS 10	Aug 23	In-process records and more frequent updates now in MEDLINE
NEWS 11	Aug 23	PAGE IMAGES FOR 1947-1966 RECORDS IN CAPLUS AND CA
NEWS 12	Aug 23	Adis Newsletters (ADISNEWS) now available on STN
NEWS 13	Sep 17	IMSworld Pharmaceutical Company Directory name change to PHARMASEARCH
NEWS 14	Oct 09	Korean abstracts now included in Derwent World Patents Index
NEWS 15	Oct 09	Number of Derwent World Patents Index updates increased
NEWS 16	Oct 15	Calculated properties now in the REGISTRY/ZREGISTRY File
NEWS 17	Oct 22	Over 1 million reactions added to CASREACT
NEWS 18	Oct 22	DGENE GETSIM has been improved
NEWS 19	Oct 29	AAASD no longer available
NEWS 20	Nov 19	New Search Capabilities USPATFULL and USPAT2
NEWS 21	Nov 19	TOXCENTER(SM) - new toxicology file now available on STN

NEWS EXPRESS	August 15 CURRENT WINDOWS VERSION IS V6.0c, CURRENT MACINTOSH VERSION IS V6.0 (ENG) AND V6.0J (JP), AND CURRENT DISCOVER FILE IS DATED 07 AUGUST 2001
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS INTER	General Internet Information
NEWS LOGIN	Welcome Banner and News Items
NEWS PHONE	Direct Dial and Telecommunication Network Access to STN
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* * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 14:30:56 ON 25 NOV 2001

=> d cluster .biotech
CLUSTER NAME CLUSTER DEFINITION
---------- ----------

.BIOTECH MEDLINE BIOSIS BIOTECHDS CAPLUS EMBASE

=> s primer# or oligo?
THIS COMMAND NOT AVAILABLE IN THE CURRENT FILE
Some commands only work in certain files. For example, the EXPAND command can only be used to look at the index in a file which has an index. Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of commands which can be used in this file.

=> s primer? or oligo?
THIS COMMAND NOT AVAILABLE IN THE CURRENT FILE
Some commands only work in certain files. For example, the EXPAND command can only be used to look at the index in a file which has an index. Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of commands which can be used in this file.

=> s primer
THIS COMMAND NOT AVAILABLE IN THE CURRENT FILE
Some commands only work in certain files. For example, the EXPAND command can only be used to look at the index in a file which has an index. Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of commands which can be used in this file.

=> file .biotech
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.80	1.80

FILE 'MEDLINE' ENTERED AT 14:38:21 ON 25 NOV 2001

FILE 'BIOSIS' ENTERED AT 14:38:21 ON 25 NOV 2001
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FILE 'BIOTECHDS' ENTERED AT 14:38:21 ON 25 NOV 2001
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=> s primer# or oligo?
L1 794928 PRIMER# OR OLIGO?

=> anneal? and each other
ANNEAL? IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s anneal? and each other
L2 1377 ANNEAL? AND EACH OTHER

=> s l1 and l2
L3 120 L1 AND L2

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 61 DUP REM L3 (59 DUPLICATES REMOVED)

=> d l4 ti

L4 ANSWER 1 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Topoisomerase and DNA ligase mediated nucleic acid ligation and molecular cloning

=> d ti l8 1-61
L8 NOT FOUND
The L-number entered has not been defined in this session, or it has been deleted. To see the L-numbers currently defined in this session, enter DISPLAY HISTORY at an arrow prompt (=>).

=> d ti l4 1-61

L4 ANSWER 1 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Topoisomerase and DNA ligase mediated nucleic acid ligation and molecular cloning

L4 ANSWER 2 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Sequence-related amplified polymorphism (SRAP), a new marker system based on a simple PCR reaction: Its application to mapping and gene tagging in Brassica

L4 ANSWER 3 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Sequencing double stranded DNA in a single set of sequencing reactions, comprises amplifying and denaturing to form single strands, which are subjected to intrastrand-**annealing** then extended, denatured and sequenced;
method is useful in clinical laboratory for diagnosing diseases, e.g. cancer

L4 ANSWER 4 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Synthesis of long double strand DNA using multiple single strand DNA templates in PCR

L4 ANSWER 5 OF 61 MEDLINE
TI Conformational analysis of a farnesyltransferase peptide inhibitor, CVIM.

L4 ANSWER 6 OF 61 MEDLINE
TI Structural study of the sodium channel inactivation gate peptide including an isoleucine-phenylalanine-methionine motif and its analogous peptide (phenylalanine/glutamine) in trifluoroethanol solutions and SDS micelles.

L4 ANSWER 7 OF 61 MEDLINE DUPLICATE 1
TI Molecular typing of Vibrio parahaemolyticus isolates, obtained from patients involved in food poisoning outbreaks in Taiwan, by random amplified polymorphic DNA analysis.

L4 ANSWER 8 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Studies on **primer**-dimer formation in polymerase chain reaction (PCR);
mechanism of DNA **primer**-dimer formation

L4 ANSWER 9 OF 61 MEDLINE DUPLICATE 2
TI Amplification of human genomic DNA sequences with polymerase chain reaction using a single **oligonucleotide primer**.

L4 ANSWER 10 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Single step assembly of multiple DNA fragments

L4 ANSWER 11 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Composite **primers** for DNA amplification

L4 ANSWER 12 OF 61 MEDLINE DUPLICATE 3
TI Solution structure of a syndecan-4 cytoplasmic domain and its interaction with phosphatidylinositol 4,5-bisphosphate.

L4 ANSWER 13 OF 61 MEDLINE DUPLICATE 4
TI Mutation detection using a novel plant endonuclease.

L4 ANSWER 14 OF 61 MEDLINE DUPLICATE 5
TI Quantitation of host cell DNA contaminate in pharmaceutical-grade plasmid DNA using competitive polymerase chain reaction and enzyme-linked immunosorbent assay.

L4 ANSWER 15 OF 61 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 6
TI Multiple-labeling of **oligonucleotide** probes for in situ hybridization.

L4 ANSWER 16 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Introducing specific mutations into double-stranded circular DNA; site-directed mutagenesis method by polymerase chain reaction with Pfu DNA-polymerase and a complementary mutagenic DNA **primer** set, **annealing**, cloning and restriction endonuclease cleavage

L4 ANSWER 17 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Sequence-specific priming of nucleic acid extension reaction; using composite DNA **primer** for DNA sequencing or RNA sequencing

L4 ANSWER 18 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Fluorescence detection assay for homogeneous PCR hybridization systems

L4 ANSWER 19 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Positive control reagents in tabletted form for PCR detection of bacteria

L4 ANSWER 20 OF 61 MEDLINE
TI Kinetics of peptide folding: computer simulations of SYPFDV and peptide variants in water.

L4 ANSWER 21 OF 61 MEDLINE DUPLICATE 7
TI Cooperative amplification of templates by cross-hybridization (CATCH).

L4 ANSWER 22 OF 61 MEDLINE DUPLICATE 8
TI Modified mRNA rescue of maternal CK1/8 mRNA depletion in Xenopus oocytes.

L4 ANSWER 23 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Method for production of cDNA libraries with anchored ends; using new DNA **primer** and DNA adaptor sets with reverse transcription-polymerase chain reaction; new subtractive hybridization method to enrich for unique cDNAs

L4 ANSWER 24 OF 61 MEDLINE DUPLICATE 9
TI Effects of modifying the tRNA(3Lys) anticodon on the initiation of human immunodeficiency virus type 1 reverse transcription.

L4 ANSWER 25 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI 'Long distance sequencer' method; a novel strategy for large DNA sequencing projects

L4 ANSWER 26 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Useful properties of restriction enzymes that recognize interrupted palindromes; restriction endonuclease BstEII for DNA ligation and application in cloning

L4 ANSWER 27 OF 61 MEDLINE

TI Folded conformations of the delta-selective opioid dermenkephalin with head-to-tail interactions. A simulated **annealing** study through NMR restraints.

L4 ANSWER 28 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Generation of a combination of mutations by use of multiple mutagenic **oligonucleotides**;
mutagenesis using 3 mutagenic **oligonucleotide** and polymerase chain reaction

L4 ANSWER 29 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Novel carrier for binding DNA;
particle adsorbent for DNA probe hybridization on surface

L4 ANSWER 30 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Increasing the size of PCR products without redesigning **primer** binding sequences;
polymerase chain reaction

L4 ANSWER 31 OF 61 MEDLINE DUPLICATE 10
TI The calf 5'- to 3'-exonuclease is also an endonuclease with both activities dependent on **primers annealed** upstream of the point of cleavage.

L4 ANSWER 32 OF 61 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 11
TI Polymorphisms in the alpha-amyl gene of wild and cultivated barley revealed by the polymerase chain reaction.

L4 ANSWER 33 OF 61 MEDLINE DUPLICATE 12
TI Genetic profiles of 12 inbred rat strains for 46 microsatellite loci selected as genetic monitoring markers.

L4 ANSWER 34 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Hybridization assay using branched nucleic acid probes

L4 ANSWER 35 OF 61 MEDLINE DUPLICATE 13
TI DNA sequencing: modular **primers** assembled from a library of hexamers or pentamers.

L4 ANSWER 36 OF 61 MEDLINE DUPLICATE 14
TI Delineation of a DNA recognition element for the vitamin D3 receptor by binding site selection.

L4 ANSWER 37 OF 61 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 15
TI Analysis of Cochliobolus carbonum races by PCR amplification with arbitrary and gene-specific **primers**.

L4 ANSWER 38 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Walking **primers** assembled from hexamers or pentamers;
hexamer and pentamer **oligonucleotide** DNA **primer** module application in DNA sequencing (conference abstract)

L4 ANSWER 39 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Preparation of chimeric humanized antibody;
mouse complementarity determining region grafting method using the polymerase chain reaction and splicing by overlap extension for use in antibody engineering

L4 ANSWER 40 OF 61 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.
TI Three-dimensional structure in solution of barwin, a protein from barley seed.

L4 ANSWER 41 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Construction of a diverse Fab expression library from autoimmunized mice

based on an improved preparation of cloning arms from bacteriophage vectors: a new library with potential for screening of biocatalysts; Fab bank construction for use in catalytic antibody screening

L4 ANSWER 42 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI New method of forming recombinant DNA;
gene splicing by overlap extension using the polymerase chain reaction; application of new recombination method to mouse major histocompatibility complex class I gene fusion construction

L4 ANSWER 43 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Use of polymerase chain reaction to detect dioxygenase genes in Pseudomonas putida;
and Escherichia coli; potential application in bioremediation (conference abstract)

L4 ANSWER 44 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Analysis of H-ras oncogene mutations in bladder carcinoma tissue DNA by allele-specific polymerase chain reaction

L4 ANSWER 45 OF 61 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 17
TI SITE-SPECIFIC MUTAGENESIS AND DNA RECOMBINATION BY USING PCR TO GENERATE RECOMBINANT CIRCLES IN-VITRO OR BY RECOMBINATION OF LINEAR PCR PRODUCTS IN-VIVO.

L4 ANSWER 46 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI DNA amplification;
for genome DNA sequencing by **annealing** of DNA **primer** and incubation with phage T7 DNA-polymerase having reduced exonuclease activity; DNA sequence

L4 ANSWER 47 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Physical properties of glycosyl diacylglycerols. 1. Calorimetric studies of a homologous series of 1,2-di-O-acyl-3-O-(.alpha.-D-glucopyranosyl)-sn-glycerols

L4 ANSWER 48 OF 61 MEDLINE DUPLICATE 18
TI Technical aspects of typing for HLA-DP alleles using allele-specific DNA in vitro amplification and sequence-specific **oligonucleotide** probes. Detection of single base mismatches.

L4 ANSWER 49 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Method and reagents for detecting nucleic acid sequences

L4 ANSWER 50 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI A method of simultaneously producing a large number of [Leu-17]vasoactive intestinal polypeptide analogs

L4 ANSWER 51 OF 61 MEDLINE DUPLICATE 19
TI Allele-specific enzymatic amplification of beta-globin genomic DNA for diagnosis of sickle cell anemia.

L4 ANSWER 52 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Sequence dependence of DNA structure. The B, Z, and A conformations of polydeoxynucleotides containing repeating units of 6 to 16 base pairs

L4 ANSWER 53 OF 61 MEDLINE DUPLICATE 20
TI A ligase-mediated gene detection technique.

L4 ANSWER 54 OF 61 MEDLINE
TI Solid-phase assembly of DNA duplexes from synthetic **oligonucleotides**.

L4 ANSWER 55 OF 61 CAPLUS COPYRIGHT 2001 ACS

TI Solid-phase assembly of DNA duplexes from synthetic **oligonucleotides**

L4 ANSWER 56 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Molecular cloning and sequence analysis of Newcastle disease virus

L4 ANSWER 57 OF 61 MEDLINE DUPLICATE 21
TI Sequence alterations in temperature-sensitive M-protein mutants (complementation group III) of vesicular stomatitis virus.

L4 ANSWER 58 OF 61 MEDLINE DUPLICATE 22
TI In vitro site-directed mutagenesis with synthetic DNA **oligonucleotides** yields unexpected deletions and insertions at high frequency.

L4 ANSWER 59 OF 61 CAPLUS COPYRIGHT 2001 ACS
TI Synthetic DNA for the production of proteins by recombinant DNA method

L4 ANSWER 60 OF 61 MEDLINE DUPLICATE 23
TI Regulation of actin polymerization by villin, a 95,000 dalton cytoskeletal component of intestinal brush borders.

L4 ANSWER 61 OF 61 MEDLINE DUPLICATE 24
TI RNA synthesis of vesicular stomatitis virus. VII. Complete separation of the mRNA's of vesicular stomatitis virus by duplex formation.

=> d ibib ab l4 4

L4 ANSWER 4 OF 61 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:197596 CAPLUS
DOCUMENT NUMBER: 132:247108
TITLE: Synthesis of long double strand DNA using multiple single strand DNA templates in PCR
INVENTOR(S): Okamoto, Yasushi; Hirai, Masana; Kajino, Tsutomu
PATENT ASSIGNEE(S): Denso Co., Ltd., Japan; Toyota Central Research and Development Laboratories, Inc.
SOURCE: Jpn. Kokai Tokkyo Koho, 10 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2000083668	A2	20000328	JP 1998-267227	19980907

AB A method of synthesizing long double strand DNA using multiple single strand DNA templates in a PCR reaction is claimed. Chem. synthesized single strand DNA templates have complementary linking/overlapping regions on either 3' or 5' end, and are capable of sequentially **annealing** to **each other** via the linking/overlapping region to form a double strand. A 3' or 5' overhang on the double strand DNA is then extended using a **primer** complementary to the overhang sequence in a PCR reaction. The **primer** is designed to have a higher melting temp. than that of single strand DNA template linking/overlapping regions. Single strand DNA template concns. are roughly equal and the **primer** concn. is 10 fold higher. Synthesis of long double strand DNA contg. unnatural nucleotide sequence is achieved. Long double strand DNAs were synthesized using 3 single strand DNA templates with 3' overhang and sep. using 4 single strand DNA templates without 5' overhang.

=> s l4 not py 2000
L5 61 L4 NOT PY 2000

=> d iall

L5 ANSWER 1 OF 61 MEDLINE
ACCESSION NUMBER: 2000451586 MEDLINE
DOCUMENT NUMBER: 20460340 PubMed ID: 11007274
TITLE: Structural study of the sodium channel inactivation gate peptide including an isoleucine-phenylalanine-methionine motif and its analogous peptide (phenylalanine/glutamine) in trifluoroethanol solutions and SDS micelles.
AUTHOR: Kuroda Y; Miyamoto K; Matsumoto M; Maeda Y; Kanaori K; Otaka A; Fujii N; Nakagawa T
CORPORATE SOURCE: Graduate School of Pharmaceutical Sciences, Kyoto University, Japan.. yokuroda@pharm.kyoto-u.ac.jp
SOURCE: JOURNAL OF PEPTIDE RESEARCH, (2000 Sep) 56 (3) 172-84. Journal code: CTZ. ISSN: 1397-002X.
PUB. COUNTRY: Denmark
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010125

ABSTRACT:
In order to gain insight into the gating mechanisms of Na+ channels, in particular their inactivation mechanisms, we studied the structures of the Na+ channel inactivation gate related peptide which includes the IFM (Ile-Phe-Met) motif (Ac-KKKFGGQDIFMTEEQKK-NH2; K1480-K1496 in rat brain type-IIA Na+ channels, MP-3A) and its F/Q(Gln) substituted one (MP-4A) in trifluoroethanol (TFE) solutions and sodium dodecyl sulfate (SDS) micelles using circular dichroism (CD) and 1H-NMR spectroscopies. Based on observed nuclear Overhauser effect constraints, three-dimensional structures of MP-3A and MP-4A were determined using simulated **annealing** molecular dynamics/ energy minimization calculations. In TFE solutions, no appreciable differences in the structure were observed using either CD or NMR spectra. In SDS micelles, however, the two peptides exhibited definitely different structures from ***each*** **other**. It was found that in MP-3A, residues 11488 and T1491 were spatially proximate with **each other** owing to hydrogen bonding between the amide proton of 11488 and the hydroxyl oxygen atom of T1491, whereas in MP-4A, F/Q substitution separated them owing to conformational changes. The solvent-accessible surfaces calculated for the structures of MP-3A and MP-4A showed that the former has a smoother interaction surface to the hydrophobic docking site than the latter. In conclusion, the conformational changes, as well as decreased hydrophobicity around the IFM motif owing to the F/Q mutation, may be one reason why F1489Q mutated channels cannot inactivate almost completely.

CONTROLLED TERM:
Amino Acid Motifs
Circular Dichroism
*Ion Channel Gating
*Isoleucine: CH, chemistry
*Methionine: CH, chemistry
Nuclear Magnetic Resonance, Biomolecular: MT, methods
***Oligopeptides: CH, chemistry**
Oligopeptides: PD, pharmacology
*Peptide Fragments: CH, chemistry
*Phenylalanine: CH, chemistry
*Sodium Channels: AI, antagonists & inhibitors
*Sodium Dodecyl Sulfate: CH, chemistry
*Trifluoroethanol: CH, chemistry
CAS REGISTRY NO.: 151-21-3 (Sodium Dodecyl Sulfate); 3617-44-5

(Phenylalanine); 7004-09-3 (Isoleucine); 7005-18-7 (Methionine); 75-89-8 (Trifluoroethanol)

CHEMICAL NAME: 0 (**Oligopeptides**); 0 (Peptide Fragments); 0 (Sodium Channels)

=> d iall l5 1-30

L5 ANSWER 1 OF 61 MEDLINE

ACCESSION NUMBER: 2000451586 MEDLINE

DOCUMENT NUMBER: 20460340 PubMed ID: 11007274

TITLE: Structural study of the sodium channel inactivation gate peptide including an isoleucine-phenylalanine-methionine motif and its analogous peptide (phenylalanine/glutamine) in trifluoroethanol solutions and SDS micelles.

AUTHOR: Kuroda Y; Miyamoto K; Matsumoto M; Maeda Y; Kanaori K; Otaka A; Fujii N; Nakagawa T

CORPORATE SOURCE: Graduate School of Pharmaceutical Sciences, Kyoto University, Japan.. yokuroda@pharm.kyoto-u.ac.jp

SOURCE: JOURNAL OF PEPTIDE RESEARCH, (2000 Sep) 56 (3) 172-84. Journal code: CTZ. ISSN: 1397-002X.

PUB. COUNTRY: Denmark

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200101

ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010125

ABSTRACT:
In order to gain insight into the gating mechanisms of Na+ channels, in particular their inactivation mechanisms, we studied the structures of the Na+ channel inactivation gate related peptide which includes the IFM (Ile-Phe-Met) motif (Ac-KKKFGGQDIFMTEEQKK-NH2; K1480-K1496 in rat brain type-IIA Na+ channels, MP-3A) and its F/Q(Gln) substituted one (MP-4A) in trifluoroethanol (TFE) solutions and sodium dodecyl sulfate (SDS) micelles using circular dichroism (CD) and 1H-NMR spectroscopies. Based on observed nuclear Overhauser effect constraints, three-dimensional structures of MP-3A and MP-4A were determined using simulated **annealing** molecular dynamics/ energy minimization calculations. In TFE solutions, no appreciable differences in the structure were observed using either CD or NMR spectra. In SDS micelles, however, the two peptides exhibited definitely different structures from ***each*** **other**. It was found that in MP-3A, residues 11488 and T1491 were spatially proximate with **each other** owing to hydrogen bonding between the amide proton of 11488 and the hydroxyl oxygen atom of T1491, whereas in MP-4A, F/Q substitution separated them owing to conformational changes. The solvent-accessible surfaces calculated for the structures of MP-3A and MP-4A showed that the former has a smoother interaction surface to the hydrophobic docking site than the latter. In conclusion, the conformational changes, as well as decreased hydrophobicity around the IFM motif owing to the F/Q mutation, may be one reason why F1489Q mutated channels cannot inactivate almost completely.

CONTROLLED TERM:
Amino Acid Motifs
Circular Dichroism
*Ion Channel Gating
*Isoleucine: CH, chemistry
*Methionine: CH, chemistry
Nuclear Magnetic Resonance, Biomolecular: MT, methods
***Oligopeptides: CH, chemistry**
Oligopeptides: PD, pharmacology
*Peptide Fragments: CH, chemistry
*Phenylalanine: CH, chemistry
*Sodium Channels: AI, antagonists & inhibitors

*Sodium Dodecyl Sulfate: CH, chemistry
*Trifluoroethanol: CH, chemistry

CAS REGISTRY NO.: 151-21-3 (Sodium Dodecyl Sulfate); 3617-44-5 (Phenylalanine); 7004-09-3 (Isoleucine); 7005-18-7 (Methionine); 75-89-8 (Trifluoroethanol)

CHEMICAL NAME: 0 (**Oligopeptides**); 0 (Peptide Fragments); 0 (Sodium Channels)

L5 ANSWER 2 OF 61 MEDLINE

ACCESSION NUMBER: 2000397344 MEDLINE

DOCUMENT NUMBER: 20273195 PubMed ID: 10815773

TITLE: Conformational analysis of a farnesyltransferase peptide inhibitor, CVIM.

AUTHOR: Carlacci L

CORPORATE SOURCE: Department of Chemistry, University of South Florida, Tampa 33620, USA.. lou@finch.cas.usf.edu

SOURCE: JOURNAL OF COMPUTER-AIDED MOLECULAR DESIGN, (2000 May) 14 (4) 369-82.
Journal code: JCB; 8710425. ISSN: 0920-654X.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200008

ENTRY DATE: Entered STN: 20000824
Last Updated on STN: 20000824
Entered Medline: 20000811

ABSTRACT:
The conformational states of the peptide Cys-Val-Ile-Met (or CVIM) were computed and characterized. CVIM inhibits farnesylation of the Ras oncogene product, p21ras, at the cysteine residue of the C-terminal segment. CVIM is active in an extended conformation. A similar peptide (KTKCVFM) appears to bind the enzyme in the Type I bend conformation. In the present study, the conformations of CVIM were computed in an aqueous environment with the peptide in the zwitterionic state. Solvation free energy based on solvent accessible surface area and a distance dependent dielectric were used in the calculations. Final conformations of multiple independent Monte Carlo simulated ***annealing*** (MCSA) conformational searches were used as starting points for Metropolis Monte Carlo (MMC) runs. Conformations saved at intervals during MMC runs were analyzed. Conformers were separated by interactive clustering in dihedral angle coordinates. The four lowest energy conformers corresponding to a Type I bend, extended, AB-bend, and BA-bend were within 0.3 kcal/mol of ***each*** **other**, and dominant in terms of population. The Type I bend and extended conformers were supported by the binding studies. The extended conformer was the most populated. In the AB-bend conformer, 'A' indicates the alpha-helix conformation of Val, and 'B' indicates the beta-strand conformation of Ile. The AB- and BA-bend conformations differed from the extended conformation in the value of Val psi and Ile psi, respectively, and from the Type I bend conformation in the value of Ile psi and Val psi, respectively. The four lowest energy conformers were characterized in terms of energy, density of low energy conformations (or entropy), structure, side chain rotamer fraction population, and interatomic distances.

CONTROLLED TERM:
Check Tags: In Vitro
*Alkyl and Aryl Transferases: AI, antagonists & inhibitors
Amino Acid Sequence
Computer Simulation
Drug Design
Electrostatics
*Enzyme Inhibitors: CH, chemistry
Enzyme Inhibitors: PD, pharmacology
***Oligopeptides: CH, chemistry**
Oligopeptides: PD, pharmacology
Protein Conformation

Proto-Oncogene Protein p21(ras): CH, chemistry
Proto-Oncogene Protein p21(ras): ME, metabolism
Thermodynamics

CHEMICAL NAME: 0 (Enzyme Inhibitors); 0 (**Oligopeptides**); 0 (cysteinyl-valyl-isoleucyl-methionine); EC 2.5 (Alkyl and Aryl Transferases); EC 2.5.1.29 (farnesyltranstransferase); EC 3.6.1.- (Proto-Oncogene Protein p21(ras))

L5 ANSWER 3 OF 61 MEDLINE
ACCESSION NUMBER: 1999262771 MEDLINE
DOCUMENT NUMBER: 99262771 PubMed ID: 10325328
TITLE: Molecular typing of Vibrio parahaemolyticus isolates, obtained from patients involved in food poisoning outbreaks in Taiwan, by random amplified polymorphic DNA analysis.
AUTHOR: Wong H C; Liu C C; Pan T M; Wang T K; Lee C L; Shih D Y
CORPORATE SOURCE: Department of Microbiology, Soochow University, Taipei, Taiwan 11102, Republic of China.. wonghc@mail.scu.edu.tw
SOURCE: JOURNAL OF CLINICAL MICROBIOLOGY, (1999 Jun) 37 (6) 1809-12.
Journal code: HSH; 7505564. ISSN: 0095-1137.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990712
Last Updated on STN: 19990712
Entered Medline: 19990623

ABSTRACT:
Vibrio parahaemolyticus is one of the most important food-borne pathogens in Taiwan, Japan, and other countries with long coastlines. This paper reports on the development of a new random amplified polymorphic DNA (RAPD) method for the molecular typing of this pathogen. The 10-mer **primer** 284 (5'-CAG GCG CAC A-3') was selected to generate polymorphic amplification profiles of the genomic DNA at an **annealing** temperature of 38 degrees C. A total of 308 clinical isolates of V. parahaemolyticus collected during food poisoning outbreaks in Taiwan, mostly occurring between 1993 and 1995, plus 11 environmental and clinical reference strains were analyzed by this RAPD method. A total of 41 polymorphic RAPD patterns were recognized, and these patterns were arbitrarily grouped into 16 types (A to P). Types A, B, C, D, and E were the major types, and subtypes C3, C5, E1, B1, D2, and A2 were the major patterns. The major types were phylogenetically more closely related to ***each*** **other** than to any of the minor types.

CONTROLLED TERM: Check Tags: Comparative Study; Human; Support, Non-U.S. Gov't
DNA, Bacterial: GE, genetics
*Disease Outbreaks
Electrophoresis, Gel, Pulsed-Field: MT, methods
*Food Poisoning: EP, epidemiology
Food Poisoning: MI, microbiology
Phylogeny
*Random Amplified Polymorphic DNA Technique
Serotyping: MT, methods
Taiwan: EP, epidemiology
Vibrio Infections: CL, classification
*Vibrio Infections: EP, epidemiology
Vibrio parahaemolyticus: CL, classification
Vibrio parahaemolyticus: GE, genetics
*Vibrio parahaemolyticus: IP, isolation & purification

CHEMICAL NAME: 0 (DNA, Bacterial)

L5 ANSWER 4 OF 61 MEDLINE
ACCESSION NUMBER: 1999200258 MEDLINE

DOCUMENT NUMBER: 99200258 PubMed ID: 10102135
TITLE: Amplification of human genomic DNA sequences with polymerase chain reaction using a single **oligonucleotide primer**.
AUTHOR: Luo L; Diamandis E P
CORPORATE SOURCE: Department of Pathology and Laboratory Medicine, Mount Sinai Hospital, Toronto, Ontario, Canada.
SOURCE: JOURNAL OF CLINICAL LABORATORY ANALYSIS, (1999) 13 (2) 69-74.
Journal code: JLA; 8801384. ISSN: 0887-8013.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990607
Last Updated on STN: 19990607
Entered Medline: 19990524

ABSTRACT:
We present two examples of exponential nucleic acid amplification with the polymerase chain reaction (PCR) in the presence of only one amplification ***primer*** . Cloning and sequencing of the PCR products generated by amplification of human genomic DNA revealed that the amplified sequence contained only one **primer** and its complement, at the two ends of the PCR product. Although these experiments were performed with **primers** derived from the sequence of the prostate specific antigen (PSA) gene and the normal epithelial cell-specific 1 gene (NES1), the amplified sequences were novel and had no homology with either PSA or NES1 DNA. While both PSA and NES1 genes reside on chromosome 19q13.3-q13.4, the amplified sequences were found by mapping to reside on chromosome 5q12 and 5p15.1-p15.3, respectively. When we examined the mechanism of amplification by PCR using one **primer** in these two cases, we found that there was a high homology between the PSA ***primer*** or the NES1 **primer** and the two regions flanking the amplified sequence of chromosome 5q12 or 5p15. This indicated that the single PSA or NES1 **primer** could **anneal** on both strands of the DNA of that region, and mediate the exponential amplification. Since this phenomenon occurred to us twice with a limited number of different PCR reactions performed in our laboratory (< 20), we believe that it may represent a common artifact of PCR. Moreover, it appears that the palindromic ***primer*** binding sites can **anneal** to **each** ***other*** forming DNA cruciforms.

CONTROLLED TERM: Check Tags: Human
Base Sequence
Chromosome Mapping
Chromosomes, Human, Pair 19
Chromosomes, Human, Pair 5
Cloning, Molecular
*DNA: AN, analysis
***DNA Primers**
Molecular Sequence Data
Neoplasm Proteins: GE, genetics
*Polymerase Chain Reaction: MT, methods
Prostate-Specific Antigen: GE, genetics
Sequence Analysis, DNA
CAS REGISTRY NO.: 9007-49-2 (DNA)
CHEMICAL NAME: 0 (DNA **Primers**); 0 (NES1 protein); 0 (Neoplasm Proteins); EC 3.4.21.77 (Prostate-Specific Antigen)

L5 ANSWER 5 OF 61 MEDLINE
ACCESSION NUMBER: 1998428637 MEDLINE
DOCUMENT NUMBER: 98428637 PubMed ID: 9753726
TITLE: Mutation detection using a novel plant endonuclease.
AUTHOR: Oleykowski C A; Bronson Mullins C R; Godwin A K; Yeung A T

CORPORATE SOURCE: Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA.
CONTRACT NUMBER: CA06927 (NCI)
CA70328 (NCI)
CA71426 (NCI)
+
SOURCE: NUCLEIC ACIDS RESEARCH, (1998 Oct 15) 26 (20) 4597-602. Journal code: O8L; 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199812
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 20000303
Entered Medline: 19981207

ABSTRACT:
We have discovered a useful new reagent for mutation detection, a novel nuclease CEL I from celery. It is specific for DNA distortions and mismatches from pH 6 to 9. Incision is on the 3'-side of the mismatch site in one of the two DNA strands in a heteroduplex. CEL I-like nucleases are found in many plants. We report here that a simple method of enzyme mutation detection using CEL I can efficiently identify mutations and polymorphisms. To illustrate the efficacy of this approach, the exons of the BRCA1 gene were amplified by PCR using **primers** 5'-labeled with fluorescent dyes of two colors. The PCR products were **annealed** to form heteroduplexes and subjected to CEL I incision. In GeneScan analyses with a PE Applied Biosystems automated DNA sequencer, two independent incision events, one in each strand, produce truncated fragments of two colors that complement **each other** to confirm the position of the mismatch. CEL I can detect 100% of the sequence variants present, including deletions, insertions and missense alterations. Our results indicate that CEL I mutation detection is a highly sensitive method for detecting both polymorphisms and disease-causing mutations in DNA fragments as long as 1120 bp in length.

CONTROLLED TERM: Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
*Apiaceae: EN, enzymology
*Base Pair Mismatch: GE, genetics
*DNA Mutational Analysis: MT, methods
Endonucleases: IP, isolation & purification
*Endonucleases: ME, metabolism
Exons: GE, genetics
*Fungal Proteins: GE, genetics
*Genes, BRCA1
Hydrogen-Ion Concentration
Nucleic Acid Heteroduplexes
Plant Components: EN, enzymology
Plant Extracts
Plant Shoots: EN, enzymology
Polymerase Chain Reaction
Polymorphism (Genetics)
Sequence Analysis, DNA
CHEMICAL NAME: 0 (FBP1 protein, fungal); 0 (Fungal Proteins); 0 (Nucleic Acid Heteroduplexes); 0 (Plant Extracts); EC 3.1.-(Endonucleases)

L5 ANSWER 6 OF 61 MEDLINE
ACCESSION NUMBER: 1998286920 MEDLINE
DOCUMENT NUMBER: 98286920 PubMed ID: 9625256
TITLE: Quantitation of host cell DNA contaminate in pharmaceutical-grade plasmid DNA using competitive polymerase chain reaction and enzyme-linked immunosorbent assay.

AUTHOR: Lahijani R; Duhon M; Lusby E; Betita H; Marquet M
CORPORATE SOURCE: Vical, Inc., San Diego, CA 92121, USA.
SOURCE: HUMAN GENE THERAPY, (1998 May 20) 9 (8) 1173-80.
Journal code: A12; 9008950. ISSN: 1043-0342.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980903
Last Updated on STN: 19980903
Entered Medline: 19980827

ABSTRACT:
The rising interest in gene therapy for the treatment of numerous disorders necessitates the need for the large-scale production of therapeutic biopharmaceuticals that meet stringent purity standards. Residual host cell DNA in recombinant pharmaceuticals has been identified as a potential risk factor that must be quantitated carefully both during the manufacturing process and in the final product. We describe a PCR method to quantitate contaminating levels of host cell DNA in clinical plasmid DNA preparations intended for human gene therapy. The quantitation is based on the coamplification of two similar templates, the target DNA and a synthetic competitor, and the quantitation of the resulting PCR products. The competitor is identical to the target DNA PCR product except for a 29-bp internal replacement. As a result, the two PCR products can easily be distinguished from **each other**. The competitive nature of the assay allows the use of the ratio of the target DNA PCR product to the competitor DNA PCR product to determine the original amount of target DNA in a sample. The **primers** used in this assay ***anneal*** to a conserved region of the E. coli 23S rRNA gene. One of the ***primers*** is biotinylated, allowing the PCR products to be detected colorimetrically after their capture on microtiter plates. The capture is accomplished by differential hybridization to target and competitor-specific probes covalently attached to wells of microtiter plates. The entire assay is performed in less than 2 hr postamplification. This method represents an attractive alternative to Southern blot analysis, which is the currently established method for DNA quantitation.

CONTROLLED TERM: Check Tags: Human
Binding, Competitive
Blotting, Southern
Cells, Cultured
*DNA: AN, analysis
DNA Restriction Enzymes
DNA, Bacterial: GE, genetics
Enzyme-Linked Immunosorbent Assay
Escherichia coli: GE, genetics
*Gene Therapy
*Plasmids: GE, genetics
*Polymerase Chain Reaction: MT, methods
Sensitivity and Specificity
Time Factors
CAS REGISTRY NO.: 9007-49-2 (DNA)
CHEMICAL NAME: 0 (DNA, Bacterial); 0 (Plasmids); EC 3.1.21 (DNA Restriction Enzymes)

L5 ANSWER 7 OF 61 MEDLINE
ACCESSION NUMBER: 1998250752 MEDLINE
DOCUMENT NUMBER: 98250752 PubMed ID: 9582338
TITLE: Solution structure of a syndecan-4 cytoplasmic domain and its interaction with phosphatidylinositol 4,5-bisphosphate.
AUTHOR: Lee D; Oh E S; Woods A; Couchman J R; Lee W
CORPORATE SOURCE: Department of Biochemistry, College of Science, Yonsei University, Seoul 120-740, Korea.
CONTRACT NUMBER: GM50194 (NIGMS)

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 May 22) 273 (21) 13022-9.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 20000303
Entered Medline: 19980625

ABSTRACT:
Syndecan-4, a transmembrane heparan sulfate proteoglycan, is a coreceptor with integrins in cell adhesion. It has been suggested to form a ternary signaling complex with protein kinase Calpha and phosphatidylinositol 4,5-bisphosphate (PIP2). Syndecans each have a unique, central, and variable (V) region in their cytoplasmic domains, and that of syndecan-4 is critical to its interaction with protein kinase C and PIP2. Two **oligopeptides** corresponding to the variable region (4V) and whole domain (4L) of syndecan-4 cytoplasmic domain were synthesized for nuclear magnetic resonance (NMR) studies. Data from NMR and circular dichroism indicate that the cytoplasmic domain undergoes a conformational transition and forms a symmetric dimer in the presence of phospholipid activator PIP2. The solution conformations of both free and PIP2-complexed 4V have been determined by two-dimensional NMR spectroscopy and dynamical simulated **annealing** calculations. The 4V peptide in the presence of PIP2 formed a compact dimer with two twisted strands packed parallel to **each other** and the exposed surface of the dimer consisted of highly charged and polar residues. The overall three-dimensional structure in solution exhibits a twisted clamp shape having a cavity in the center of dimeric interface. In addition, it has been observed that the syndecan-4V strongly interacts not only with fatty acyl groups but also the anionic head group of PIP2. These findings reveal that PIP2 promotes ***oligomerization*** of syndecan-4 cytoplasmic domain for transmembrane signaling and cell-matrix adhesion.

CONTROLLED TERM: Check Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Amino Acid Sequence
Circular Dichroism
*Cytoplasm: CH, chemistry
Dimerization
Magnetic Resonance Spectroscopy
*Membrane Glycoproteins: CH, chemistry
Molecular Sequence Data
*Phosphatidylinositol 4,5-Diphosphate: CH, chemistry
Protein Conformation
*Proteoglycans: CH, chemistry
Solutions
CHEMICAL NAME: 0 (Membrane Glycoproteins); 0 (Phosphatidylinositol 4,5-Diphosphate); 0 (Proteoglycans); 0 (Solutions); 0 (syndecan-4)

L5 ANSWER 8 OF 61 MEDLINE
ACCESSION NUMBER: 97467426 MEDLINE
DOCUMENT NUMBER: 97467426 PubMed ID: 9325101
TITLE: Kinetics of peptide folding: computer simulations of SYPFDV and peptide variants in water.
AUTHOR: Mohanty D; Elber R; Thirumalai D; Beglov D; Roux B
CORPORATE SOURCE: The Fritz Haber Research Center for Molecular Dynamics and The Wolfson Center for Applied Structural Biology, The Hebrew University, Jerusalem, 91904, Israel.
CONTRACT NUMBER: GM41905 (NIGMS)
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1997 Sep 26) 272 (3) 423-42.
Journal code: J6V; 2985088R. ISSN: 0022-2836.

PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199710
ENTRY DATE: Entered STN: 19971224
Last Updated on STN: 19971224
Entered Medline: 19971028

ABSTRACT:
The folding of Ser-Tyr-Pro-Phe-Asp-Val (SYPFDV), and sequence variants of this peptide (SYPYD and SYPFD) are studied computationally in an explicit water environment. An atomically detailed model of the peptide is embedded in a sphere of TIP3P water molecules and its optimal structure is computed by simulated **annealing**. At distances from the peptide that are beyond a few solvation shells, a continuum solvent model is employed. The simulations are performed using a mean field approach that enhances the efficiency of sampling peptide conformations. The computations predict a small number of conformations as plausible folded structures. All have a type VI turn conformation for the peptide backbone, similar to that found using NMR. However, some of the structures differ from the experimentally proposed ones in the packing of the proline ring with the aromatic residues. The second most populated structure has, in addition to a correctly folded backbone, the same hydrophobic packing as the conformation measured by NMR.Our simulations suggest a kinetic mechanism that consists of three separate stages. The time-scales associated with these stages are distinct and depend differently on temperature. Electrostatic interactions play an initial role in guiding the peptide chain to a roughly correct structure as measured by the end-to-end distance. At the same time or later the backbone torsions rearrange due to local tendency of the proline ring to form a turn: this step depends on solvation forces and is helped by loose hydrophobic interactions. In the final step, hydrophobic residues pack against **each other**.We also show the existence of an off the pathway intermediate, suggesting that even in the folding of a small peptide "misfolded" structures can form. The simulations clearly show that parallel folding paths are involved.Our findings suggest that the process of peptide folding shares many of the features expected for the significantly larger protein molecules.
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CONTROLLED TERM: Check Tags: Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
*Computer Simulation
Electrostatics
Kinetics
Models, Chemical
*Models, Molecular
***Oligopeptides: CH, chemistry**
Protein Conformation
*Protein Folding
Research Design
Temperature
Vacuum
Water: CH, chemistry
CAS REGISTRY NO.: 7732-18-5 (Water)
CHEMICAL NAME: 0 (**Oligopeptides**)

L5 ANSWER 9 OF 61 MEDLINE
ACCESSION NUMBER: 97448854 MEDLINE
DOCUMENT NUMBER: 97448854 PubMed ID: 9303179
TITLE: Modified mRNA rescue of maternal CK1/8 mRNA depletion in Xenopus oocytes.
AUTHOR: Raats J M; Gell D; Vickers L; Heasman J; Wylie C
CORPORATE SOURCE: Department of Biochemistry, University of Nijmegen, The Netherlands.

SOURCE: ANTISENSE AND NUCLEIC ACID DRUG DEVELOPMENT, (1997 Aug) 7 (4) 263-77.
Journal code: CJY; 9606142. ISSN: 1087-2906.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199802
ENTRY DATE: Entered STN: 19980217
Last Updated on STN: 19980217
Entered Medline: 19980205

ABSTRACT:
This work addresses two issues, the use of antisense ***oligodeoxynucleotides*** to deplete specific mRNAs in Xenopus oocytes to analyze their functions during development and the role of cytokeratin filaments in cells of the early Xenopus embryo. We have shown previously that depletion of cytokeratin CK1/8 mRNA causes defects in the early embryo. In this study, we show that the **oligos**, modified with phosphoramidate linkages to improve stability, are capable of degrading exogenous mRNA up to 27 hours after injection in the oocyte. For this reason, the phenotype could not be rescued by injection of a synthetic CK1/8 mRNA. However, modification of the synthetic CK1/8 mRNA, which prevents **annealing** of the antisense ***oligonucleotide*** used for depleting the endogenous CK1/8 mRNA, did result in the rescue of the CK1/8 depletion phenotype. These results demonstrate that the phenotype observed after depletion of the CK1/8 mRNA is truly caused by the lack of CK1/8 protein. Injection of the closely related type II cytokeratin (CK55) did not result in the same level of rescue of the CK1/8 depletion phenotype, suggesting that structurally similar members of the cytokeratin family, expressed at different stages of development, cannot substitute for **each other** in the early embryo.

CONTROLLED TERM: Check Tags: Animal; Female; Support, Non-U.S. Gov't
Amino Acid Sequence
Amino Acid Substitution
Base Sequence
Blastomeres: DE, drug effects
Blastomeres: PH, physiology
Embryo, Nonmammalian: DE, drug effects
*Embryo, Nonmammalian: PH, physiology
*Genomic Imprinting
*Keratin: BI, biosynthesis
Keratin: GE, genetics
Molecular Sequence Data
Mutagenesis, Site-Directed
***Oligonucleotides, Antisense*: PD, pharmacology**
Oocytes: DE, drug effects
*Oocytes: PH, physiology
*RNA, Messenger: DE, drug effects
RNA, Messenger: GE, genetics
RNA, Messenger: ME, metabolism
Xenopus laevis
CAS REGISTRY NO.: 68238-35-7 (Keratin)
CHEMICAL NAME: 0 (**Oligonucleotides**, Antisense); 0 (RNA, Messenger)

L5 ANSWER 10 OF 61 MEDLINE
ACCESSION NUMBER: 97182621 MEDLINE
DOCUMENT NUMBER: 97182621 PubMed ID: 9030760
TITLE: Cooperative amplification of templates by cross-hybridization (CATCH).
AUTHOR: Ehricht R; Ellinger T; McCaskill J S
CORPORATE SOURCE: Department of Molecular Information Processing, Institute of Molecular Biotechnology, Jena, Germany.. rehr@imb-jena.de

SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1997 Jan 15) 243 (1-2) 358-64.
Journal code: EMZ; 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199703
ENTRY DATE: Entered STN: 19970327
Last Updated on STN: 19980206
Entered Medline: 19970320

ABSTRACT:
In vitro amplification systems not only serve as a tool for the processing of DNA, but have also provided important model systems for the investigation of fundamental issues in evolutionary optimization. In this work we present a coupled amplification system based on the self-sustained sequence replication (3SR), also known as nucleic acid sequence-based amplification (NASBA), which allows the experimental investigation of evolving molecular cooperation. The 3SR reaction is an isothermal method of nucleic acid amplification and an alternative to PCR. A target nucleic acid sequence can be amplified exponentially in vitro using two enzymes: reverse transcriptase (RT) and a DNA-dependent RNA polymerase (RNAP). A system has been constructed in which amplification of two molecular species is cooperatively coupled. These species are single-stranded (ss)DNA templates (D1 and D2) of lengths 58 and 68 nucleotides, respectively. Coupling occurs when D1 and D2 **anneal** to ***each*** **other** via a complementary region (DB and DB') situated at the 3' end of each template. RT elongates the hybridized templates producing a double-stranded (ds)DNA of 106 base pairs (bp). This double strand contains two promoters, which are situated on either side of, and directly adjacent to DB, and which are oriented towards **each other**. These promoters specify two RNA transcripts encompassing, respectively, the D1 and D2 portion of the dsDNA. After hybridization of two **primers** (P1 and P2) to the transcripts (R1 and R2) and reverse transcription, the ss templates D1 and D2 are regenerated. Amplification cycles of D1 and D2 are coupled cooperatively via the common dsDNA intermediate. Under optimized batch conditions the system shows the expected growth phases: exponential, linear and saturation phase. The enzymes of the 3SR cycle tend to misincorporate nucleotides and to produce abortive products. In future experiments, we intend to use the system for studies of evolutionary processes in spatially distributed systems where new strategies for optimization at the molecular level are possible.

CONTROLLED TERM: Check Tags: Support, Non-U.S. Gov't
DNA-Directed RNA Polymerase: ME, metabolism
*Evolution, Molecular
Kinetics
Nucleic Acid Conformation
Nucleic Acid Hybridization
Promoter Regions (Genetics)
RNA-Directed DNA Polymerase: ME, metabolism
Templates
CHEMICAL NAME: EC 2.7.7.49 (RNA-Directed DNA Polymerase); EC 2.7.7.6 (DNA-Directed RNA Polymerase)

L5 ANSWER 11 OF 61 MEDLINE
ACCESSION NUMBER: 96383294 MEDLINE
DOCUMENT NUMBER: 96383294 PubMed ID: 8791158
TITLE: Folded conformations of the delta-selective opioid dermenkephalin with head-to-tail interactions. A simulated **annealing** study through NMR restraints.
AUTHOR: Naim M; Nicolas P; Baron D
CORPORATE SOURCE: Peptide Bioactivation Laboratory, Jacques Monod Institute, University of Paris 7, France.
SOURCE: INTERNATIONAL JOURNAL OF PEPTIDE AND PROTEIN RESEARCH,

(1996 May) 47 (5) 353-60.
Journal code: GSD; 0330420. ISSN: 0367-8377.
PUB. COUNTRY: Denmark
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961203

ABSTRACT:
Despite similar tripeptide N-termini, dermorphin (Tyr-D-Ala-Phe-Gly-Tyr-Pro-Ser-NH2) and dermenkephalin (Tyr-D-Met-Phe-His-Leu-Met-Asp-NH2), naturally occuring opioid peptides from frog skin, exhibit high affinity but contrasting selectivity for the mu- and delta-opioid receptors, respectively. Structure-activity relationship studies have shown that the N-terminal tripeptide, Tyr-D-Xaa-Phe (where Xaa is either Ala or Met), is necessary for binding with both the mu- and delta-receptors while the nature and/or the conformation of the C-terminus His-Leu-Met-Asp-NH2 of dermenkephalin are responsible for addressing the peptide to the delta-receptor. In order to examine the conformational characteristics that are related to the selectivity of dermenkephalin towards the delta-receptor, 50 NOE restraints (10 between non-adjacent residues), and 7 dihedral angles, derived from a two-dimensional 1H-NMR study of dermenkephalin in dimethyl sulfoxide, were used in simulated ***annealing*** and energy minimization procedures. Twenty-four resulting conformers (60% of the generated structures) with no severe distance restraint violation were pooled into seven groups and three related families. These 24 conformers show close proximity between the two methionine residues, S-shaped structures, mean planes of N-terminal and C-terminal moieties almost at right angles to **each other**, a C-terminus region above the plane of the N-terminal region and g- as preferential orientation in the side chain of Phe. Aside these similarities, families of conformers differ by the preferential orientation in the side chain of Tyr (t or g-) and proximity between Tyr and Asp, or Tyr and the C-terminus. In contrast to previous models, practically no beta-turn structures exist for dermenkephalin, most of the NH hydrogen bonds participating to gamma-turns. The possible relationship between the conformational characteristics of dermenkephalin and the delta-opioid receptor selectivity is discussed.

CONTROLLED TERM: Check Tags: Animal; Support, Non-U.S. Gov't
Anura
Magnetic Resonance Spectroscopy
***Oligopeptides: CH, chemistry**
Protein Conformation
Protein Folding
CAS REGISTRY NO.: 119975-64-3 (deltorphin)
CHEMICAL NAME: 0 (**Oligopeptides**)

L5 ANSWER 12 OF 61 MEDLINE
ACCESSION NUMBER: 96256782 MEDLINE
DOCUMENT NUMBER: 96256782 PubMed ID: 8676496
TITLE: Effects of modifying the tRNA(3Lys) anticodon on the initiation of human immunodeficiency virus type 1 reverse transcription.
AUTHOR: Huang Y; Shalom A; Li Z; Wang J; Mak J; Wainberg M A; Kleiman L
CORPORATE SOURCE: Lady Davis Institute for Medical Research and McGill AIDS Centre, McGill University, Montreal, Quebec, Canada.
SOURCE: JOURNAL OF VIROLOGY, (1996 Jul) 70 (7) 4700-6.
Journal code: KCV; 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 199608
ENTRY DATE: Entered STN: 19960822
Last Updated on STN: 19970203
Entered Medline: 19960815

ABSTRACT:
tRNA(3Lys) is a **primer** for reverse transcription in human immunodeficiency virus type 1 (HIV-1), and the anticodon of tRNA(3Lys) has been implicated in playing a role in both its placement onto the HIV-1 genome and its interaction with HIV-1 reverse transcriptase (RT). In this work, the anticodon in a tRNA(3Lys) gene was changed from UUU to CUA (tRNA(3Lys)Su+) or, in addition, G-73 was altered to A (tRNA(3Lys)Su+G73A). COS-7 cells were transfected with either wild-type or mutant tRNA(3Lys) genes, and both the wild-type and mutant tRNA(3Lys) produced were purified by using immobilized tRNA-specific hybridization probes. Each mutant tRNA(3Lys) was tested for its ability to prime reverse transcription in vitro, either alone or in competition with wild-type tRNA(3Lys). Short RT extensions of wild-type and mutant tRNALys could be distinguished from **each other** by their different mobilities in one-dimensional single-stranded conformation polymorphism polyacrylamide gel electrophoresis. These reverse transcription products show that heat-**annealed** tRNA(3Lys)Su+ has the same ability as heat-***annealed*** wild-type tRNA(3Lys) to prime RT and competes equally well with wild-type tRNA(3Lys) for priming RT. tRNA(3Lys)Su+G73A has 60% of the wild-type ability to prime RT but competes poorly with wild-type tRNA(3Lys) for priming RT. However, the priming abilities of wild-type and mutant tRNA(3) are quite different when in vivo-placed tRNA is examined. HIV-1 produced in COS cells transfected with a plasmid containing both the HIV-1 proviral DNA and DNA coding for tRNA(3Lys)Su+ contains both endogenous, cellular wild-type tRNA(3Lys) and mutant tRNA(3Lys). When total viral RNA is used as the source of ***primer*** tRNA placed onto the genomic RNA in vivo, only wild-type tRNA(3Lys) is used as a **primer**. If the total viral RNA is first heated and exposed to hybridizing conditions, then both the wild-type and mutant tRNA(3Lys) act as **primers** for RT. These results indicate that the tRNA(3Lys)Su+ packaged into the virions is unable to act as a ***primer*** for RT, and a model is proposed to explain the disparate results between heat-**annealed** and in vivo-placed **primer** tRNA.

CONTROLLED TERM: Check Tags: Human; Support, Non-U.S. Gov't
*Anticodon
Base Sequence
DNA Probes
*HIV-1: GE, genetics
HIV-1: PH, physiology
Molecular Sequence Data
Mutation
Nucleic Acid Conformation
RNA
*RNA, Transfer, Amino Acyl: GE, genetics
RNA, Transfer, Amino Acyl: IP, isolation & purification
RNA, Viral
*Transcription, Genetic: GE, genetics
Virion
Virus Assembly
CAS REGISTRY NO.: 63231-63-0 (RNA)
CHEMICAL NAME: 0 (Anticodon); 0 (DNA Probes); 0 (RNA **primers**); 0 (RNA, Transfer, Amino Acyl); 0 (RNA, Viral); 0 (tRNA, lysine-)

L5 ANSWER 13 OF 61 MEDLINE
ACCESSION NUMBER: 94164226 MEDLINE
DOCUMENT NUMBER: 94164226 PubMed ID: 8119335
TITLE: Genetic profiles of 12 inbred rat strains for 46 microsatellite loci selected as genetic monitoring markers.
AUTHOR: Hirayama N; Kuramoto T; Kondo Y; Yamada J; Serikawa T
CORPORATE SOURCE: Institute of Laboratory Animals, Faculty of Medicine, Kyoto

University, Japan.
SOURCE: JIKKEN DOBUTSU. EXPERIMENTAL ANIMALS, (1994 Jan) 43 (1) 129-32.
Journal code: EOH; 1256412. ISSN: 0007-5124.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199404
ENTRY DATE: Entered STN: 19940412
Last Updated on STN: 19940412
Entered Medline: 19940405

ABSTRACT:
Genetic profiles for 46 microsatellite loci of 12 inbred strains of rats, including 2 congenic strains and a coisogenic strain, have been demonstrated. Rates of loci with different alleles between 2 inbred strains, which are not closely related to **each other** in origin, were from 71.7% between ACI/N and IS/Kyo strains to 41.3% between F344/N and TM/Kyo. On the other hand, the rates were 0% in both of 2 sets of congenic strains; between F344/N and F344/N-rnu, or between BN/fMaiKyo and BN.IS. When WTC/Kyo and the coisogenic strain TRM/Kyo (WTC/Kyo-tm) were compared for 115 microsatellite loci, no loci with different alleles between the strains were found. The 46 loci should be useful as genetic monitoring markers, since all of the ***primer*** pairs generate distinct PCR-products at a fixed ***annealing*** temperature of 55 degrees C.

CONTROLLED TERM: Check Tags: Animal; Support, Non-U.S. Gov't
Alleles
Animals, Laboratory
*Chromosome Mapping
*Genetic Markers
Polymerase Chain Reaction
Rats
*Rats, Inbred Strains: GE, genetics
CHEMICAL NAME: 0 (Genetic Markers)

L5 ANSWER 14 OF 61 MEDLINE
ACCESSION NUMBER: 94117427 MEDLINE
DOCUMENT NUMBER: 94117427 PubMed ID: 8288581
TITLE: The calf 5'- to 3'-exonuclease is also an endonuclease with both activities dependent on **primers annealed** upstream of the point of cleavage.
AUTHOR: Murante R S; Huang L; Turchi J J; Bambara R A
CORPORATE SOURCE: Department of Biochemistry, University of Rochester School of Medicine and Dentistry, New York 14642.
CONTRACT NUMBER: GM24441 (NIGMS)
T32-GM07102 (NIGMS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1994 Jan 14) 269 (2) 1191-6.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199402
ENTRY DATE: Entered STN: 19940312
Last Updated on STN: 19940312
Entered Medline: 19940222

ABSTRACT:
The catalytic activity of the calf thymus 5'- to 3'-exonuclease was measured on substrates consisting of two **primers annealed** adjacent to ***each*** **other** on a template. Exonucleolytic degradation of the downstream **primer** is very slow if the **primers** are separated by a gap of one nucleotide or if no upstream **primer** is present. When

only a nick separates the **primers**, degradation is rapid. This suggests that the nuclease is designed to work with calf DNA polymerases such that synthesis from an upstream **primer** creates the favored nuclease substrate. Nuclease action then destroys the substrate, but it is regenerated by further polymerization. This process, termed nick translation, is necessary for both DNA replication and repair. If the downstream **primer** has an unannealed 5'-region, that region is removed by an endonuclease activity residing in the same enzyme. Efficient endonuclease action also requires an upstream **primer** that is **annealed** such that its 3'-end is directly adjacent to the **annealed** region of the downstream ***primer*** . This reaction is likely to be important for removal of DNA segments that are damaged such that exonuclease cleavage of the damaged site is not possible.

CONTROLLED TERM: Check Tags: Animal; Support, U.S. Gov't, P.H.S.
Base Sequence
Cattle
DNA Primers: CH, chemistry
DNA Repair
DNA Replication
*Endonucleases: ME, metabolism
*Exonucleases: ME, metabolism
Molecular Sequence Data
Substrate Specificity

CHEMICAL NAME: 0 (DNA **Primers**); EC 3.1.- (Endonucleases); EC 3.1.- (Exonucleases)

L5 ANSWER 15 OF 61 MEDLINE
ACCESSION NUMBER: 93249449 MEDLINE
DOCUMENT NUMBER: 93249449 PubMed ID: 8387288
TITLE: Delineation of a DNA recognition element for the vitamin D3 receptor by binding site selection.
AUTHOR: Perez-Fernandez R; Arce V; Freedman L P
CORPORATE SOURCE: Dept. of Physiology, University of Santiago School of Medicine, Santiago de Compostela, Spain.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1993 Apr 30) 192 (2) 728-37.
Journal code: 9Y8; 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199306
ENTRY DATE: Entered STN: 19930618
Last Updated on STN: 19930618
Entered Medline: 19930601

ABSTRACT:
The vitamin D3 receptor is a ligand-inducible transcriptional regulatory protein. The receptor modulates the transcription of target genes by binding directly to specific DNA sites, termed vitamin D response elements; these sites vary considerably in their homologies to **each other**. In order to approach the question of what sequences can constitute high affinity recognition elements for the vitamin D3 receptor, we have selected for such sites in vitro by mixing overexpressed and purified vitamin D3 receptor DNA binding domain with an **oligonucleotide** duplex pool containing a completely randomized central region flanked by **primer-** ***annealing*** sites. Following multiple rounds of immunoprecipitation and amplification by PCR to enrich for high affinity sites, individual clones were sequenced and found to contain nearly identical hexameric sequences, yielding a consensus 5'-AGGGGG-3'. This sequence is similar to some known vitamin D3 receptor binding sites, such as osteocalcin, but quite divergent from others. This suggests that the vitamin D3 receptor may be able to selectively recognize at least two classes of sequence elements.

CONTROLLED TERM: Check Tags: Animal; Human; Support, Non-U.S. Gov't
Antibodies: IM, immunology
Base Sequence
Binding Sites
*Cholecalciferol: ME, metabolism
Cloning, Molecular
*DNA: ME, metabolism
Molecular Sequence Data
Receptors, Calcitriol
Receptors, Steroid: GE, genetics
Receptors, Steroid: IM, immunology
*Receptors, Steroid: ME, metabolism
Sequence Alignment
CAS REGISTRY NO.: 67-97-0 (Cholecalciferol); 9007-49-2 (DNA)
CHEMICAL NAME: 0 (Antibodies); 0 (Receptors, Calcitriol); 0 (Receptors, Steroid)

L5 ANSWER 16 OF 61 MEDLINE
ACCESSION NUMBER: 93248265 MEDLINE
DOCUMENT NUMBER: 93248265 PubMed ID: 8483939
TITLE: DNA sequencing: modular **primers** assembled from a library of hexamers or pentamers.
AUTHOR: Kotler L E; Zevin-Sonkin D; Sobolev I A; Beskin A D; Ulanovsky L E
CORPORATE SOURCE: Department of Structural Biology, Weizmann Institute of Science, Rehovot, Israel.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1993 May 1) 90 (9) 4241-5.
Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199306
ENTRY DATE: Entered STN: 19930618
Last Updated on STN: 19930618
Entered Medline: 19930601

ABSTRACT:
Here we report a striking effect displayed by "modular **primers,**" which consist of hexamer or pentamer **oligonucleotide** modules base-stacked to **each other** upon **annealing** to a DNA template. Such a combination of modules is found to prime DNA sequencing reactions uniquely, unlike either of the modules alone. We attribute this effect in part to the increase in the affinity of an **oligonucleotide** for the template in the presence of an adjacent module. All possible pentamer (or hexamer) sequences total 1024 (or 4096) samples, a manageable size for a presynthesized library. This approach can replace the synthesis of ***primers*** , which is the current bottleneck in time and cost of the ***primer*** walking sequencing, and can allow full automation of the closed cycle of walking.

CONTROLLED TERM: *Base Sequence
DNA: CH, chemistry
*DNA: GE, genetics
DNA, Viral: CH, chemistry
DNA, Viral: GE, genetics
*Databases, Factual
Molecular Sequence Data
***Oligodeoxyribonucleotides**
Oligodeoxyribonucleotides: CS, chemical synthesis
Templates
CAS REGISTRY NO.: 9007-49-2 (DNA)
CHEMICAL NAME: 0 (DNA, Viral); 0 (**Oligodeoxyribonucleotides**)

L5 ANSWER 17 OF 61 MEDLINE
ACCESSION NUMBER: 90278110 MEDLINE
DOCUMENT NUMBER: 90278110 PubMed ID: 2191042
TITLE: Technical aspects of typing for HLA-DP alleles using allele-specific DNA in vitro amplification and sequence-specific **oligonucleotide** probes. Detection of single base mismatches.
AUTHOR: Fugger L; Morling N; Ryder L P; Odum N; Svejgaard A
CORPORATE SOURCE: Department of Clinical Immunology, State University Hospital, Copenhagen, Denmark.
SOURCE: JOURNAL OF IMMUNOLOGICAL METHODS, (1990 May 25) 129 (2) 175-85.
Journal code: IFE; 1305440. ISSN: 0022-1759.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199007
ENTRY DATE: Entered STN: 19900824
Last Updated on STN: 19900824
Entered Medline: 19900717

ABSTRACT:
The polymerase chain reaction (PCR) is an effective method for in vitro DNA amplification which combined with probing with synthetic ***oligonucleotides*** can be used for, e.g., HLA-typing. We have studied the technical aspects of HLA-DP typing with the technique. DNA from mononuclear nucleated cells was extracted with either a simple salting out method or phenol/chloroform. Both DNAs could be readily used for PCR. The MgC2 concentration of the PCR buffer and the **annealing** temperature of the thermal cycle of the PCR were the two most important variables. The MgCl2 concentration and the temperature must be carefully titrated for each ***primer*** pair in the PCR. The influence of mismatches between the ***primer*** and the DNA template were studied and we found that, by using ***primers*** differing only from **each other** at the 3' end, cross-amplification of closely homologous alleles could be avoided. Thus, single base mismatches may be detected in the PCR and typing for HLA-DP gene variants, which differ for only one base, may be performed.

CONTROLLED TERM: Check Tags: Human; Support, Non-U.S. Gov't
Alleles
Amino Acid Sequence
Base Sequence
DNA Probes, HLA
Genetic Techniques
*HLA-DP Antigens: GE, genetics
Magnesium Chloride
Molecular Sequence Data
Nucleic Acid Hybridization
Polymerase Chain Reaction
Temperature
Variation (Genetics)
CAS REGISTRY NO.: 7786-30-3 (Magnesium Chloride)
CHEMICAL NAME: 0 (DNA Probes, HLA); 0 (HLA-DP Antigens)

L5 ANSWER 18 OF 61 MEDLINE
ACCESSION NUMBER: 89202405 MEDLINE
DOCUMENT NUMBER: 89202405 PubMed ID: 2704745
TITLE: Allele-specific enzymatic amplification of beta-globin genomic DNA for diagnosis of sickle cell anemia.
AUTHOR: Wu D Y; Ugozzoli L; Pal B K; Wallace R B
CORPORATE SOURCE: Department of Molecular Biochemistry, Beckman Research Institute of the City of Hope, Duarte, CA 91010.
CONTRACT NUMBER: CA33572 (NCI)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE

UNITED STATES OF AMERICA, (1989 Apr) 86 (8) 2757-60.
Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198905
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 19970203
Entered Medline: 19890524

ABSTRACT:
A rapid nonradioactive approach to the diagnosis of sickle cell anemia is described based on an allele-specific polymerase chain reaction (ASPCR). This method allows direct detection of the normal or the sickle cell beta-globin allele in genomic DNA without additional steps of probe hybridization, ligation, or restriction enzyme cleavage. Two allele-specific ***oligonucleotide*** **primers**, one specific for the sickle cell allele and one specific for the normal allele, together with another ***primer*** complementary to both alleles were used in the polymerase chain reaction with genomic DNA templates. The allele-specific **primers** differed from **each other** in their terminal 3' nucleotide. Under the proper **annealing** temperature and polymerase chain reaction conditions, these **primers** only directed amplification on their complementary allele. In a single blind study of DNA samples from 12 individuals, this method correctly and unambiguously allowed for the determination of the genotypes with no false negatives or positives. If ASPCR is able to discriminate all allelic variation (both transition and transversion mutations), this method has the potential to be a powerful approach for genetic disease diagnosis, carrier screening, HLA typing, human gene mapping, forensics, and paternity testing.

CONTROLLED TERM: Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
Alleles
*Anemia, Sickle Cell: DI, diagnosis
Fluorescent Dyes
*Gene Amplification
*Globins: GE, genetics
Oligonucleotide Probes
CAS REGISTRY NO.: 9004-22-2 (Globins)
CHEMICAL NAME: 0 (Fluorescent Dyes); 0 (**Oligonucleotide** Probes)

L5 ANSWER 19 OF 61 MEDLINE
ACCESSION NUMBER: 88321655 MEDLINE
DOCUMENT NUMBER: 88321655 PubMed ID: 3413476
TITLE: A ligase-mediated gene detection technique.
AUTHOR: Landegren U; Kaiser R; Sanders J; Hood L
CORPORATE SOURCE: Division of Biology, California Institute of Technology, Pasadena 91125.
SOURCE: SCIENCE, (1988 Aug 26) 241 (4869) 1077-80.
Journal code: UJ7; 0404511. ISSN: 0036-8075.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198809
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19980206
Entered Medline: 19880923

ABSTRACT:
An assay for the presence of given DNA sequences has been developed, based on the ability of two **oligonucleotides** to **anneal** immediately adjacent to **each other** on a complementary target DNA molecule. The two **oligonucleotides** are then joined covalently by the

action of a DNA ligase, provided that the nucleotides at the junction are correctly base-paired. Thus single nucleotide substitutions can be distinguished. This strategy permits the rapid and standardized identification of single-copy gene sequences in genomic DNA.

CONTROLLED TERM: Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.
Amino Acid Sequence
Base Sequence
Cell Line
*DNA: AN, analysis
DNA: GE, genetics
DNA: ME, metabolism
*DNA Ligases: ME, metabolism
DNA, Recombinant: ME, metabolism
Fluorescent Dyes
Globins: GE, genetics
Molecular Sequence Data
Nucleic Acid Denaturation
Nucleic Acid Hybridization
Polymorphism (Genetics)
*Polynucleotide Ligases: ME, metabolism
CAS REGISTRY NO.: 9004-22-2 (Globins); 9007-49-2 (DNA)
CHEMICAL NAME: 0 (DNA, Recombinant); 0 (Fluorescent Dyes); EC 6.5.1. (Polynucleotide Ligases); EC 6.5.1.- (DNA Ligases)

L5 ANSWER 20 OF 61 MEDLINE
ACCESSION NUMBER: 88096656 MEDLINE
DOCUMENT NUMBER: 88096656 PubMed ID: 3697135
TITLE: Solid-phase assembly of DNA duplexes from synthetic **oligonucleotides.**
AUTHOR: Hostomsky Z; Smrt J
CORPORATE SOURCE: Institute of Molecular Genetics, Czechoslovak Academy of Sciences, Prague.
SOURCE: NUCLEIC ACIDS SYMPOSIUM SERIES, (1987) (18) 241-4.
Journal code: O8N; 8007206. ISSN: 0261-3166.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198801
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19900305
Entered Medline: 19880127

ABSTRACT:
A new method of rapid and efficient assembly of extended DNA duplexes in solid phase was developed. Subassemblies of separately **annealed** ***oligonucleotides*** were stepwise hybridized to **each** ***other*** on a solid support. Two types of supports with anchor ***oligonucleotide*** were tested: Fractosil-1000 with **oligo**-dT sequence and Sephacryl S-500 with an **oligonucleotide** bound via CNBr-activation procedure. Sephacryl S-500 turned out to be the support of choice since all enzymatic reactions of the assembly procedure (phosphorylation, ligation, restriction enzyme digestion) could be efficiently performed with DNA immobilized on Sephacryl S-500 particles.

CONTROLLED TERM: Acrylic Resins
*DNA: CS, chemical synthesis
*Genes, Synthetic
Indicators and Reagents
***Oligodeoxyribonucleotides: CS, chemical synthesis**
Oligodeoxyribonucleotides: IP, isolation & purification
CAS REGISTRY NO.: 9007-49-2 (DNA)

CHEMICAL NAME: 0 (Acrylic Resins); 0 (Indicators and Reagents); 0 (**Oligodeoxyribonucleotides**); 0 (Sephacryl Superfine)

L5 ANSWER 21 OF 61 MEDLINE
ACCESSION NUMBER: 86062892 MEDLINE
DOCUMENT NUMBER: 86062892 PubMed ID: 2999421
TITLE: Sequence alterations in temperature-sensitive M-protein mutants (complementation group III) of vesicular stomatitis virus.
AUTHOR: Gopalakrishna Y; Lenard J
CONTRACT NUMBER: AI-13003 (NIAID)
SOURCE: JOURNAL OF VIROLOGY, (1985 Dec) 56 (3) 655-9.
Journal code: KCV; 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M11754
ENTRY MONTH: 198601
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19970203
Entered Medline: 19860102

ABSTRACT:
Sequences were determined of the coding regions of the M-protein genes of the Glasgow and Orsay strains of vesicular stomatitis virus (Indiana serotype) and of two group III (M-protein) mutants derived from each wild type. Synthetic ***primers*** were **annealed** with viral genomic RNA and extended with reverse transcriptase. The resulting high-molecular-weight cDNA was sequenced directly. Both Glasgow and Orsay wild types differed in 13 bases from a clone of the San Juan strain sequenced by J. K. Rose and C. J. Gallione (J. Virol. 39:519-528, 1981). Six of these base changes caused amino acid changes in each wild type, whereas seven were degenerate. The Orsay and Glasgow sequences resembled **each other** more closely than either resembled that of Rose and Gallione, differing in eight nucleotides and four amino acids. Each of the four mutants, however, differed from its parent wild type in only one or two point mutations. Every mutation caused a change either from or to a charged amino acid; the change for tsG31 was Lys (position 215) to Glu, the change for tsO23 was Gly (position 21) to Glu, the change for tsO89 was Ala (position 133) to Asp, the changes for tsG33 were Lys (position 204) to Thr and Glu (position 214) to Lys. The charge differences predicted from these amino acid changes was confirmed by nonequilibrium pH gradient electrophoresis for tsG31, tsG33, tsO23, and the two wild types. These mutations affect residues spanning nearly 85% of the linear sequence, although the mutants possess nearly identical phenotypic properties.

CONTROLLED TERM: Check Tags: Support, U.S. Gov't, P.H.S.
Amino Acid Sequence
Base Sequence
DNA: GE, genetics
Isoelectric Point
Mutation
Structure-Activity Relationship
Temperature
*Vesicular Stomatitis-Indiana Virus: GE, genetics
*Viral Proteins: GE, genetics
CAS REGISTRY NO.: 9007-49-2 (DNA)
CHEMICAL NAME: 0 (Viral Proteins)

L5 ANSWER 22 OF 61 MEDLINE
ACCESSION NUMBER: 84169502 MEDLINE
DOCUMENT NUMBER: 84169502 PubMed ID: 6324090
TITLE: In vitro site-directed mutagenesis with synthetic DNA **oligonucleotides** yields unexpected deletions and insertions at high frequency.

AUTHOR: Osinga K A; Van der Bliek A M; Van der Horst G; Groot Koerkamp M J; Tabak H F; Veeneman G H; Van Boom J H
SOURCE: NUCLEIC ACIDS RESEARCH, (1983 Dec 20) 11 (24) 8595-608. Journal code: O8L; 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198405
ENTRY DATE: Entered STN: 19900319
Last Updated on STN: 19990129
Entered Medline: 19840511

ABSTRACT:
We have used in vitro site-directed mutagenesis with synthetic DNA ***oligonucleotides*** to introduce single nucleotide mutations in yeast mtDNA. In addition to the expected DNA alterations we also recovered with high frequency mutants with large deletions and insertions which arose through interaction with the synthetic DNA fragment. Characterization of a number of these by DNA sequence analysis has permitted reconstruction of the mutagenic events. In all cases, the DNA fragment had base paired with non-adjacent DNA sequences sometimes more than 1000 nucleotides apart from **each** ***other*** on the target strand. The products of such interactions cannot be avoided due to the non-stringent **annealing** conditions during complementary DNA strand synthesis. However, deliberate mispairing can be directed precisely, as shown by our ability to specifically delete the 1143-bp intron from the yeast mitochondrial gene coding for large ribosomal RNA with a synthetic DNA fragment consisting of the sequence of the exon borders flanking the intron.

CONTROLLED TERM: Check Tags: Comparative Study; Support, Non-U.S. Gov't
Base Composition
Base Sequence
*Chromosome Deletion
Coliphages: GE, genetics
*DNA Transposable Elements: DE, drug effects
*DNA, Mitochondrial: GE, genetics
DNA, Recombinant
Escherichia coli: GE, genetics
*Genes, Fungal: DE, drug effects
*Mutation
Nucleic Acid Hybridization
***Oligodeoxyribonucleotides: PD, pharmacology**
***Oligonucleotides: PD, pharmacology**
Saccharomyces cerevisiae: DE, drug effects
*Saccharomyces cerevisiae: GE, genetics
CHEMICAL NAME: 0 (DNA Transposable Elements); 0 (DNA, Mitochondrial); 0 (DNA, Recombinant); 0 (**Oligodeoxyribonucleotides**); 0 (**Oligonucleotides**)

L5 ANSWER 23 OF 61 MEDLINE
ACCESSION NUMBER: 81112142 MEDLINE
DOCUMENT NUMBER: 81112142 PubMed ID: 6893953
TITLE: Regulation of actin polymerization by villin, a 95,000 dalton cytoskeletal component of intestinal brush borders.
AUTHOR: Craig S W; Powell L D
SOURCE: CELL, (1980 Dec) 22 (3) 739-46. Journal code: CQ4; 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198104
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19900316

Entered Medline: 19810413

ABSTRACT:
A 95,000 dalton actin-binding polypeptide, villin, has been purified to 98% homogeneity from brush border cytoskeletons of chicken intestinal epithelial cells. In vitro, this protein exerts control over the polymerization of actin. In the presence of villin, the lag phase preceding detectable actin polymerization is shortened and the steady state equilibrium viscosity is reduced in proportion to the amount of villin present. A molar ratio of villin:actin of 1:40 results in a 70% reduction of the Ostwald viscosity. Significant effects can be detected at a ratio of 1:600. These ratios are physiologically relevant because the ratio of villin:actin in brush borders is 1:13 and in isolated microvilli is 1:9-12. Reduction of viscosity is mirrored by an increase in the amount of protein which fails to sediment at 150,000 X g for 60 min. An assay of the nonsedimentable protein for actin monomers by the inhibition of DNAase I showed that the concentration of monomer was not significantly altered by the presence of villin. Electron microscopic examination of negatively stained, nonsedimentable actin demonstrated that the presence of villin during actin polymerization results in the production of short **oligomers** which cannot **anneal** with **each** ***other*** to form long filaments. Villin is also effective in reducing the viscosity of F-actin when it is added to a fuly polymerized actin sample. In view of these striking properties, villin is likely to be an important in vivo regulator of cytoskeletal structure and, by implication, of cell shape and motility.

CONTROLLED TERM: Check Tags: Animal; Support, U.S. Gov't, P.H.S.
*Actins: ME, metabolism
Carrier Proteins: IP, isolation & purification
*Carrier Proteins: ME, metabolism
*Cell Membrane: UL, ultrastructure
Chickens
*Cytoskeleton: ME, metabolism
Intestinal Mucosa: UL, ultrastructure
*Microvilli: UL, ultrastructure
Molecular Weight

CHEMICAL NAME: 0 (Actins); 0 (Carrier Proteins); 0 (villin)

L5 ANSWER 24 OF 61 MEDLINE

ACCESSION NUMBER: 77144287 MEDLINE
DOCUMENT NUMBER: 77144287 PubMed ID: 191636
TITLE: RNA synthesis of vesicular stomatitis virus. VII. Complete separation of the mRNA's of vesicular stomatitis virus by duplex formation.
AUTHOR: Freeman G J; Rose J K; Clinton G M; Huang A S
SOURCE: JOURNAL OF VIROLOGY, (1977 Mar) 21 (3) 1094-104.
Journal code: KCV; 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197705
ENTRY DATE: Entered STN: 19900313
Last Updated on STN: 19900313
Entered Medline: 19770527

ABSTRACT:
Full-length virion RNA and complementary mRNA's of vesicular stomatitis virus can be **annealed** to **each other**, digested with RNases, and then separated as five unique duplex RNA molecules on polyacrylamide slab gels. Similar RNA duplexes were detected whether mRNA or virion RNA was the radioactive component and whether the mRNA was synthesized in vitro or in vivo. The sharp banding pattern of these RNA molecules was dependent on treatment with RNase T2, suggesting that removal of poly(A) is necessary. Identification of the coding region contained in each RNA duplex was based on their previous identification as single-stranded mRNA on

formamide-containing, polyacrylamide gels. Because the two smallest mRNA'S had not been previously separated, their identification was based on their in vitro transcriptional gene order. In the order of increasing mobilities on the slab gels, the RNA duplexes are identified as the hybrid of the region of the genome RNA hybridized to the complementary mRNA coding for the large protein, the glycoprotein, the nucleocapsid protein, the core-associated NS protein, and the matrix protein (L,G,N,NS, and M). Several lines of evidence support the presence of undegraded complete mRNA, excluding poly(A), in these RNA duplexes. Also, the two smallest mRNA's, separated by duplex formation, were denatured, and their individual **oligonucleotide** fingerprints were determined. From chemical length determinations, the molecular weights of the mRNA, minus poly(A), are 2.78 X 10(5) and 2.5 X 10(5), respectively, for the mRNA's of the NS and M proteins.

CONTROLLED TERM: Check Tags: Support, U.S. Gov't, P.H.S.
Cell Line
Molecular Weight
Nucleic Acid Denaturation
Nucleic Acid Hybridization
Oligonucleotides: AN, analysis
*RNA, Messenger: AN, analysis
RNA, Messenger: BI, biosynthesis
*RNA, Viral: AN, analysis
RNA, Viral: BI, biosynthesis
Ribonucleases: ME, metabolism
*Vesicular Stomatitis-Indiana Virus: AN, analysis
Vesicular Stomatitis-Indiana Virus: ME, metabolism

CHEMICAL NAME: 0 (**Oligonucleotides**); 0 (RNA, Messenger); 0 (RNA, Viral); EC 3.1.- (Ribonucleases)

L5 ANSWER 25 OF 61 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1999:31580 BIOSIS
DOCUMENT NUMBER: PREV199900031580
TITLE: Multiple-labeling of **oligonucleotide** probes for in situ hybridization.
AUTHOR(S): Sasaki, Junzo (1); Yamamoto, Hitoshi; Nomura, Takako; Matsuura, Junko; Seno, Masaharu; Sato, Eisuke F.; Inoue, Masayasu
CORPORATE SOURCE: (1) Dep. Anatomy, Okayama Univ. Med. Sch., 2-5-1 Shikatacho, Okayama 700-8558 Japan
SOURCE: Acta Histochemica et Cytochemica, (1998) Vol. 31, No. 4, pp. 275-279.
ISSN: 0044-5991.
DOCUMENT TYPE: Article
LANGUAGE: English
ABSTRACT:
We describe here a method to synthesize probes for in situ hybridization. This method provides more efficient incorporation of the reporter molecules such as 35S-UTP or digoxigenin-UTP Into the **oligonucleotide** probes than other methods. Two 99-base **oligonucleotides** complementary to **each** ***other*** were obtained as purified and lyophilized products (>99%). These ***oligonucleotides*** were designed as follows. The sequence of 77 bases derived from reported cDNA sequence in the literature was flanked by the restriction sites of EcoR I and Hind III (6 bases for each) with extended random sequences of 5 bases at both ends (total 99 bases). Both ***oligonucleotides*** were then **annealed** and digested with EcoR I and Hind III. The gel-purified EcoR I/Hind III-cut DNA fragment was cloned into the pGEM4Z vector. The resultant plasmid DNA was linearized with EcoR I or Hind III and used as a template for the synthesis of labeled sense or antisense riboprobes. The amelogenin probes prepared by this method clearly distinguished the localized expression of mRNA when applied to in situ hybridization.
CONCEPT CODE: Biochemical Methods - General *10050
Cytology and Cytochemistry - General *02502
Biochemical Studies - General *10060

INDEX TERMS: Major Concepts
Methods and Techniques
INDEX TERMS: Chemicals & Biochemicals
amelogenin
INDEX TERMS: Methods & Equipment
in situ hybridization: analytical method;
oligonucleotide probes multi-labeling method:
synthetic method

L5 ANSWER 26 OF 61 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1995:63693 BIOSIS
DOCUMENT NUMBER: PREV199598077993
TITLE: Polymorphisms in the alpha-amy1 gene of wild and cultivated barley revealed by the polymerase chain reaction.
AUTHOR(S): Weining, S. (1); Ko, L.; Henry, R. J.
CORPORATE SOURCE: (1) Queensland Agric. Biotechnol. Cent., Gehrmann Lab., Univ. Queensland, QLD 4072 Australia
SOURCE: Theoretical and Applied Genetics, (1994) Vol. 89, No. 4, pp. 509-513.
ISSN: 0040-5752.
DOCUMENT TYPE: Article
LANGUAGE: English
ABSTRACT:
alpha-Amylases are the key enzymes involved in the hydrolysis of starch in plants. The polymerase chain reaction (PCR) was used to detect polymorphisms in the length of amplified sequences between the **annealing** sites of two ***primers*** derived from published alpha-amy1 gene sequences in barley. These two **primers** (Bsw1 and Bsw7), flanking the promoter region and the first exon, amplified two PCR fragments in barley. One of the amplified products, with the expected length of 820 bp, appeared together with another shorter PCR band of around 750 bp. This 750-bp fragment seems to be derived from an alpha-amylase gene not reported previously. Both of the PCR products could be amplified from the two-rowed barley varieties tested, including cv Himalaya from which the sequence information was obtained. Five of the six-rowed barley varieties also have the two PCR fragments whereas another two have only the long fragment. These two fragments seem to be unique to barley, neither of them could be amplified from other cereals; for example, wheat, rye or sorghum. These two alpha-amylase fragments were mapped to the long arm of 6H, the location of the alpha-amy1 genes, using wheat-barley addition lines. Amplification of genomic DNA from wild barley accessions with **primers** Bsw1 and Bsw7 indicated that both of the fragments could be present, or the long and short fragments could be present alone. The results also demonstrated that the genes specifying these two fragments could be independent from ***each*** **other** in barley. The conserved banding pattern of these two fragments in the two-rowed barley varieties implies that artificial selection from these genes may have played an important role in the evolution of cultivated barley from wild barley.
CONCEPT CODE: Evolution *01500
Genetics and Cytogenetics - Plant *03504
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biochemical Studies - Carbohydrates 10068
Biophysics - Molecular Properties and Macromolecules 10506
Enzymes - Methods 10804
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
BIOSYSTEMATIC CODE: Gramineae *25305
INDEX TERMS: Major Concepts
Enzymology (Biochemistry and Molecular Biophysics); Evolution and Adaptation; Genetics
INDEX TERMS: Chemicals & Biochemicals

ALPHA-AMYLASE; EC 3.2.1.1; STARCH
INDEX TERMS: Miscellaneous Descriptors
ALPHA-AMYLASE EC 3.2.1.1; DNA POLYMORPHISM; EVOLUTION; STARCH
ORGANISM: Super Taxa
Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae
ORGANISM: Organism Name
Gramineae (Gramineae)
ORGANISM: Organism Superterms
angiosperms; monocots; plants; spermatophytes; vascular plants
REGISTRY NUMBER: 9000-90-2 (ALPHA-AMYLASE)
9000-90-2 (EC 3.2.1.1)
9005-25-8 (STARCH)

L5 ANSWER 27 OF 61 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1993:279115 BIOSIS
DOCUMENT NUMBER: PREV199396009340
TITLE: Analysis of Cochliobolus carbonum races by PCR amplification with arbitrary and gene-specific **primers**.
AUTHOR(S): Jones, Margaret J. (1); Dunkle, Larry D.
CORPORATE SOURCE: (1) U.S. Dep. Agric., Agric. Res. Serv., Purdue Univ., West Lafayette, IN 47907-1155 USA
SOURCE: Phytopathology, (1993) Vol. 83, No. 4, pp. 366-370.
ISSN: 0031-949X.
DOCUMENT TYPE: Article
LANGUAGE: English
ABSTRACT:
The pathogenic races of Cochliobolus carbonum cause necrotic lesions of characteristic sizes and shapes on maize (Zea mays) leaves. To distinguish the races at the molecular level, isolates of C. carbonum races as well as other related species were analyzed by PCR (polymerase chain reaction) amplification of genomic DNA using either arbitrary **oligonucleotide primers** or **primers** with homology to sequences within the Tox2 locus, which is essential for production of a host-specific toxin. Amplification products from isolates of the four pathogenic races of C. carbonum were very similar to ***each*** **other** and to those from species thought to be closely related but were substantially different from nonpathogenic race 0 and from most other species. One of the arbitrary **primers** tested distinguished isolates of C. carbonum race 3 by the absence of two amplification products present in the other pathogenic races. The patterns of amplification products from races 2 and 4 were indistinguishable with the **primers** tested, suggesting that the recently described race 4 is not substantially different from race 2. **Primers** from the Tox2 locus distinguished race 1 isolates from isolates of other races. Only isolates of race 1 contained a single amplification product of the expected length when these **primers** were used under stringent **annealing** conditions. The results indicate that PCR amplification with arbitrary **primers** or gene-specific ***primers*** is useful for differentiating the races of C. carbonum and for examining their origins.
CONCEPT CODE: Genetics and Cytogenetics - Plant *03504
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biophysics - Molecular Properties and Macromolecules *10506
Agronomy - Grain Crops *52504
Phytopathology - Diseases Caused by Fungi *54502
BIOSYSTEMATIC CODE: Ascomycetes 15100
Gramineae *25305
INDEX TERMS: Major Concepts
Agronomy (Agriculture); Biochemistry and Molecular Biophysics; Genetics; Infection

the concentration of **primers** decreases, while the concentrations of **primer**-dimer, target DNA and non-specific background product increase with an increase in PCR cycle number until the 35th cycle. The **primer**-dimer and DNA participate to form more background product between the 35th and 40th cycles. Further observations led to the proposed mechanistic model, which provides a kinetic description of the **primer**-dimer formation process with Taq DNA-polymerase (EC-2.7.7.7), the 2 **primers** and the dNTPs as the starting materials. In the first reaction, **primer** 1 and **primer** 2 **anneal** to **each other** reversibly to form a **primer** 1-**primer** 2 complex. Changing the reaction temp can shift the equilibrium for this reaction. Reaction 2 is an enzyme-substrate complex formation, which is usually reversible. Once this complex is formed, the polymerase enzyme adds the dNTPs to the 3' end to complete the **primer**-dimer. The impact of this **primer**-dimer formation on the selectivity and yield of PCR processes is discussed. (5 ref)

CLASSIFICATION: A GENETIC ENGINEERING AND FERMENTATION; A1 Nucleic Acid Technology

CONTROLLED TERMS: DNA **PRIMER**-DIMER FORMATION, POLYMERASE CHAIN REACTION, MECHANISTIC MODEL DNA AMPLIFICATION (VOL.18, NO.25)

L5 ANSWER 29 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
ACCESSION NUMBER: 2000-13505 BIOTECHDS
TITLE: Sequencing double stranded DNA in a single set of sequencing reactions, comprises amplifying and denaturing to form single strands, which are subjected to intrastrand-**annealing** then extended, denatured and sequenced;
method is useful in clinical laboratory for diagnosing diseases, e.g. cancer
AUTHOR: Gupte J; Oliphant A
PATENT ASSIGNEE: Myriad-Genet.
LOCATION: Salt Lake City, UT, USA.
PATENT INFO: US 6087099 11 Jul 2000
APPLICATION INFO: US 1997-925277 8 Sep 1997
PRIORITY INFO: US 1997-925277 8 Sep 1997
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2000-531338 [48]
ABSTRACT: A double stranded DNA (I) is claimed. The method involves amplifying (A1) (performed by polymerase chain reaction, strand displacement amplification, thermophilic strand displacement amplification) (I) using a pair of DNA **primers** to form amplified DNA by cycle sequencing, where each strand of the amplified DNA contains a first region and a second region which are reverse complements to **each other**, denaturing the amplified DNA to form single strands of DNA, allowing intrastrand-**annealing** of single strands of DNA, where first region and second region of strand gets **annealed** to form intrastrand-**annealed** DNA, extending the intrastrand-**annealed** DNA to yield panhandle DNA which upon denaturation yields a single stranded DNA containing sequence of both strands of (I), and sequencing the single stranded DNA using a sequencing **primer** to obtain sequence data containing sequences for both strands of (I). The method is useful in clinical laboratories for diagnosing diseases such as cancer which is associated with specific mutations in the gene being analyzed. (10pp)
CLASSIFICATION: A GENETIC ENGINEERING AND FERMENTATION; A1 Nucleic Acid Technology; D PHARMACEUTICALS; D7 Clinical Genetic Techniques
CONTROLLED TERMS: DS DNA AMPLIFICATION, DNA **PRIMER**, DNA DENATURATION, SS INTRASTRAND-**ANNEALING**, DNA EXTENSION, BOTH STRAND DNA SEQUENCING, APPL. CLINICAL LABORATORY DIAGNOSIS, E.G. CANCER, SPECIFIC GENE MUTATION DNA SEQUENCE POLYMERASE CHAIN REACTION STRAND DISPLACEMENT AMPLIFICATION TUMOR (VOL.19, NO.24)

L5 ANSWER 30 OF 61 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
ACCESSION NUMBER: 1999-14306 BIOTECHDS
TITLE: Studies on **primer**-dimer formation in polymerase chain reaction (PCR);
mechanism of DNA **primer**-dimer formation
AUTHOR: Das S; Mohapatra S C; *Hsu J T
CORPORATE SOURCE: Univ.Lehigh
LOCATION: Department of Chemical Engineering, Lehigh University, Bethlehem, PA 18015, USA.
Email: jth0@lehigh.edu
SOURCE: Biotechnol.Tech.; (1999) 13, 10, 643-46
CODEN: BTECE6
ISSN: 0951-208X
DOCUMENT TYPE: Journal
LANGUAGE: English
ABSTRACT: A mechanism for DNA **primer**-dimer formation during polymerase chain reaction (PCR) is proposed based on experimental results. Initial experiments demonstrated that

INDEX TERMS: Industry
crop industry
INDEX TERMS: Miscellaneous Descriptors
AGRICULTURE; GENOMIC DNA; POLYMERASE CHAIN REACTION; RACE DIFFERENTIATION
ORGANISM: Super Taxa
Ascomycetes: Fungi, Plantae; Fungi - Unspecified: Fungi, Plantae; Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae; Plantae - Unspecified: Plantae
ORGANISM: Organism Name
fungus (Fungi - Unspecified); plant (Plantae - Unspecified); Cochliobolus carbonum (Ascomycetes); Zea mays (Gramineae)
ORGANISM: Organism Superterms
angiosperms; fungi; microorganisms; monocots; nonvascular plants; plants; spermatophytes; vascular plants

L5 ANSWER 28 OF 61 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1992:450931 BIOSIS
DOCUMENT NUMBER: BA94:92331
TITLE: SITE-SPECIFIC MUTAGENESIS AND DNA RECOMBINATION BY USING PCR TO GENERATE RECOMBINANT CIRCLES IN-VITRO OR BY RECOMBINATION OF LINEAR PCR PRODUCTS IN-VIVO.
AUTHOR(S): JONES D H; WINISTORFER S C
CORPORATE SOURCE: DEP. PEDIATR., COLL. MED., UNIV. IOWA, IOWA CITY, IOWA 52242.
SOURCE: METHODS (ORLANDO), (1991) 2 (1), 2-10.
CODEN: MTHDE9. ISSN: 1046-2023.
FILE SEGMENT: BA; OLD
LANGUAGE: English
ABSTRACT:
This article describes two methods in which the polymerase chain reaction (PCR) is used for site-specific mutagenesis and for DNA recombination without any enzymatic reaction in vitro apart from DNA amplification. The first method generates DNA joints in vitro by using separate PCR amplification to generate products that when combined, denatured, and reannealed form double-stranded DNA with single-stranded ends. These single-stranded ends are designed to ***anneal*** to **each other** to yield circles, an application termed recombinant circle PCR (RCPCR). RCPCR-generated DNA circles form without restriction enzyme digestion or ligation and can be transfected directly into Escherichia coli. The second method generated DNA joints in vivo by using the polymerase chain reaction to add homologous ends to DNA. Following transfection of the linear PCR product(s) into strains of E. coli used routinely in cloning, recombination of these homologous ends in vivo permits cloning of the mutant or recombinant of interest. The second method, termed recombination PCR (RPCR), diminished the number of **primers** necessary to generate a given mutant or recombinant to half that necessary in RCPCR, because it eliminates the need to generate staggered ends in vitro.
CONCEPT CODE: Cytology and Cytochemistry - Animal *02506
Genetics and Cytogenetics - Animal *03506
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Enzymes - Methods *10804
Physiology and Biochemistry of Bacteria *31000
Genetics of Bacteria and Viruses *31500
In Vitro Studies, Cellular and Subcellular 32600
BIOSYSTEMATIC CODE: Enterobacteriaceae 06702
INDEX TERMS: Miscellaneous Descriptors
ESCHERICHIA-COLI POLYMERASE CHAIN REACTION

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 NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Dec 17  The CA Lexicon available in the CAPLUS and CA files
 NEWS  3  Feb 06  Engineering Information Encompass files have new names
 NEWS  4  Feb 16  TOXLINE no longer being updated
 NEWS  5  Apr 23  Search Derwent WPINDEX by chemical structure
 NEWS  6  Apr 23  PRE-1967 REFERENCES NOW SEARCHABLE IN CAPLUS AND CA
 NEWS  7  May 07  DGENE Reload
 NEWS  8  Jun 20  Published patent applications (A1) are now in USPATFULL
 NEWS  9  JUL 13  New SDI alert frequency now available in Derwent's
                  DWPI and DPCI
 NEWS 10  Aug 23  In-process records and more frequent updates now in
                  MEDLINE
 NEWS 11  Aug 23  PAGE IMAGES FOR 1947-1966 RECORDS IN CAPLUS AND CA
 NEWS 12  Aug 23  Adis Newsletters (ADISNEWS) now available on STN
 NEWS 13  Sep 17  IMSworld Pharmaceutical Company Directory name change
                  to PHARMASEARCH
 NEWS 14  Oct 09  Korean abstracts now included in Derwent World Patents
                  Index
 NEWS 15  Oct 09  Number of Derwent World Patents Index updates increased
 NEWS 16  Oct 15  Calculated properties now in the REGISTRY/ZREGISTRY File
 NEWS 17  Oct 22  Over 1 million reactions added to CASREACT
 NEWS 18  Oct 22  DGENE GETSIM has been improved
 NEWS 19  Oct 29  AAASD no longer available
 NEWS 20  Nov 19  New Search Capabilities  USPATFULL and USPAT2
 NEWS 21  Nov 19  TOXCENTER(SM) - new toxicology file now available on STN

 NEWS EXPRESS  August 15 CURRENT WINDOWS VERSION IS V6.0c,
               CURRENT MACINTOSH VERSION IS V6.0 (ENG) AND V6.0J (JP),
               AND CURRENT DISCOVER FILE IS DATED 07 AUGUST 2001
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defined in the current session.

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=> d his

     (FILE 'HOME' ENTERED AT 15:19:18 ON 25 NOV 2001)

=> d l5 ti
NO L# DEFINED

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                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.30       0.30

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=> s primer# or oligo?
L1      794928 PRIMER# OR OLIGO?

=> s anneal? and each other
L2        1377 ANNEAL? AND EACH OTHER

=> s l1 and l2
L3         120 L1 AND L2

=> s l3 not py>2000
L4         118 L3 NOT PY>2000

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5          59 DUP REM L4 (59 DUPLICATES REMOVED)

=> d iall l5 31-59

L5   ANSWER 31 OF 59     MEDLINE                          DUPLICATE 12
ACCESSION NUMBER:    94164226     MEDLINE
DOCUMENT NUMBER:     94164226   PubMed ID: 8119335
TITLE:               Genetic profiles of 12 inbred rat strains for 46
                     microsatellite loci selected as genetic monitoring markers.
AUTHOR:              Hirayama N; Kuramoto T; Kondo Y; Yamada J; Serikawa T
CORPORATE SOURCE:    Institute of Laboratory Animals, Faculty of Medicine, Kyoto
                     University, Japan.
SOURCE:              JIKKEN DOBUTSU. EXPERIMENTAL ANIMALS, (1994 Jan) 43 (1)
                     129-32.
                     Journal code: EOH; 1256412. ISSN: 0007-5124.
```

PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199404
ENTRY DATE: Entered STN: 19940412
Last Updated on STN: 19940412
Entered Medline: 19940405

ABSTRACT:
Genetic profiles for 46 microsatellite loci of 12 inbred strains of rats, including 2 congenic strains and a coisogenic strain, have been demonstrated. Rates of loci with different alleles between 2 inbred strains, which are not closely related to **each other** in origin, were from 71.7% between ACI/N and IS/Kyo strains to 41.3% between F344/N and TM/Kyo. On the other hand, the rates were 0% in both of 2 sets of congenic strains; between F344/N and F344/N-rnu, or between BN/fMaiKyo and BN.IS. When WTC/Kyo and the coisogenic strain TRM/Kyo (WTC/Kyo-tm) were compared for 115 microsatellite loci, no loci with different alleles between the strains were found. The 46 loci should be useful as genetic monitoring markers, since all of the ***primer*** pairs generate distinct PCR-products at a fixed ***annealing*** temperature of 55 degrees C.

CONTROLLED TERM: Check Tags: Animal; Support, Non-U.S. Gov't
Alleles
Animals, Laboratory
*Chromosome Mapping
*Genetic Markers
Polymerase Chain Reaction
Rats
*Rats, Inbred Strains: GE, genetics
CHEMICAL NAME: 0 (Genetic Markers)

L5 ANSWER 32 OF 59 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1993:575379 CAPLUS
DOCUMENT NUMBER: 119:175379
TITLE: Hybridization assay using branched nucleic acid probes
INVENTOR(S): Hogan, James John; Arnold, Lyle John, Jr.; Nelson, Norman Charles; Bezverkov, Robert
PATENT ASSIGNEE(S): Gen-Probe Inc., USA
SOURCE: Eur. Pat. Appl., 58 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
INT. PATENT CLASSIF.:
MAIN: C12Q001-68
CLASSIFICATION: 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 552931	A1	19930728	EP 1993-300377	19930120
EP 552931	B1	20000524		
R: CH, DE, FR, GB, IT, LI, SE				
US 5424413	A	19950613	US 1992-940652	19920904
WO 9315102	A1	19930805	WO 1993-US486	19930121
W: AU, CA, JP, KR				
AU 9335866	A1	19930901	AU 1993-35866	19930121
AU 665062	B2	19951214		
JP 07503139	T2	19950406	JP 1993-513301	19930121
US 5451503	A	19950919	US 1994-255553	19940607
PRIORITY APPLN. INFO.:			US 1992-827021	19920122
			WO 1993-US486	19930121

ABSTRACT:
The title hybridization probes contg. .gtoreq.2 target nucleic acid-specific regions and arm regions which are complementary to the arm regions of another probes, which arms do not hybridize to **each other** in the absence of the target nucleic acid. In the presence of the targets, the probes will **anneal** to the targets and to the complementary arms of other probes to form a branched structure. The amt. of target nucleic acid can be detd. by detecting the formation of the resultant structure after the hybridization of the arm regions which involves cleavage by resolvase or S1 nuclease or restriction endonuclease, DNA footprint anal., gel electrophoresis, or use and chem. modification of intercalating agent (e.g. acridinium ester). The arm region of the probes optionally contains an extending single-stranded region for the formation of .gtoreq.1 secondary arms, contains a duplex region to serve as **primer** for DNA polymerase or as promoter for an RNA polymerase, contains a DNA/RNA duplex susceptible to RNase H cleavage, or contains a site adjacent to the duplex nucleic acid which is cleavable by Fe-EDTA or phenanthroline. With the method, a target rRNA (of Neisseria gonorrhoeae) was clearly distinguished from the potentially cross-reacting target nucleic acid with 2 mismatches (of Neisseria meningitidis).

SUPPL. TERM: nucleic acid hybridization branched probe

INDEX TERM: Genetic methods
(DNA footprint anal., for detection of target nucleic acid, with branched nucleic acid structure-forming probes)

INDEX TERM: Phosphorothioates
ROLE: BIOL (Biological study)
(branched nucleic acid structure-forming **oligonucleotide** probes contg., for nucleic acid hybridization anal.)

INDEX TERM: Nucleic acid hybridization
(branched nucleic acid structure-forming **oligonucleotide** probes for)

INDEX TERM: Mycobacterium tuberculosis
(detection of, by nucleic acid hybridization with branched nucleic acid structure-forming probes)

INDEX TERM: Neisseria gonorrhoeae
(distinguish of, from Neisseria meningitidis, by nucleic acid hybridization with branched nucleic acid structure-forming probes)

INDEX TERM: Enzymes
ROLE: BIOL (Biological study)
(DNA-resolving, cleavage, detection of target nucleic acids with branched structure-forming probes in relation to)

INDEX TERM: Leukemia
(chronic myelocytic, detection of, by nucleic acid hybridization with branched nucleic acid structure-forming probes)

INDEX TERM: Virus, animal
(human immunodeficiency 1, detection of, by nucleic acid hybridization with branched nucleic acid structure-forming probes)

INDEX TERM: Molecular association
(intercalation, agents, in detection of target nucleic acid by nucleic acid hybridization with branched nucleic acid structure-forming probes)

INDEX TERM: 150363-48-7 150363-49-8 150363-50-1 150363-51-2
ROLE: USES (Uses)
(branched nucleic acid structure-forming **oligonucleotide** probe, for detecting HIV-1)

INDEX TERM: 150363-41-0 150363-42-1 150363-43-2 150363-44-3
150363-45-4 150363-46-5 150363-47-6
ROLE: USES (Uses)

(branched nucleic acid structure-forming **oligonucleotide** probe, for detecting chronic myelogenous leukemia)

INDEX TERM: 150363-29-4 150363-30-7 150363-37-4 150363-52-3 150363-53-4 150363-54-5
ROLE: USES (Uses)
(branched nucleic acid structure-forming **oligonucleotide** probe, for detecting Mycobacterium tuberculosis)

INDEX TERM: 150363-33-0 150363-34-1 150363-35-2 150363-36-3 150363-38-5 150363-39-6 150363-40-9 150363-55-6 150363-56-7
ROLE: USES (Uses)
(branched nucleic acid structure-forming **oligonucleotide** probe, for detecting Neisseria gonorrhoeae)

INDEX TERM: 13598-51-1, Phosphorothioic acid, biological studies
7440-50-8D, Copper, complexes with phenanthroline
ROLE: BIOL (Biological study)
(branched nucleic acid structure-forming probe contg., for detn. of target nucleic acid)

INDEX TERM: 150363-31-8 150363-32-9
ROLE: USES (Uses)
(branched nucleic acid structure-forming probe, for detecting Mycobacterium tuberculosis)

INDEX TERM: 9012-90-2, DNA polymerase 9014-24-8, RNA polymerase
ROLE: USES (Uses)
(branched nucleic acid structure-forming probes contg. duplex region as **primer** for, detn. of target nucleic acid in relation to)

INDEX TERM: 60-00-4D, Fe complex 66-71-7, 1,10-Phenanthroline
ROLE: USES (Uses)
(chem. cleavage by, detn. of target nucleic acid with branched nucleic acid structure-forming probe in relation to)

INDEX TERM: 22559-71-3D, Acridinium, esters
ROLE: USES (Uses)
(cleavage by, detection of target nucleic acids with branched structure-forming probes in relation to)

INDEX TERM: 9050-76-4, RNase H 9075-08-5, DNA restriction endonuclease 37288-25-8, S1 Nuclease
ROLE: USES (Uses)
(cleavage, detection of target nucleic acids with branched structure-forming probes in relation to)

L5 ANSWER 33 OF 59 MEDLINE DUPLICATE 13
ACCESSION NUMBER: 93248265 MEDLINE
DOCUMENT NUMBER: 93248265 PubMed ID: 8483939
TITLE: DNA sequencing: modular **primers** assembled from a library of hexamers or pentamers.
AUTHOR: Kotler L E; Zevin-Sonkin D; Sobolev I A; Beskin A D; Ulanovsky L E
CORPORATE SOURCE: Department of Structural Biology, Weizmann Institute of Science, Rehovot, Israel.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1993 May 1) 90 (9) 4241-5.
Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199306
ENTRY DATE: Entered STN: 19930618
Last Updated on STN: 19930618

Entered Medline: 19930601

ABSTRACT:
Here we report a striking effect displayed by "modular **primers**," which consist of hexamer or pentamer **oligonucleotide** modules base-stacked to **each other** upon **annealing** to a DNA template. Such a combination of modules is found to prime DNA sequencing reactions uniquely, unlike either of the modules alone. We attribute this effect in part to the increase in the affinity of an **oligonucleotide** for the template in the presence of an adjacent module. All possible pentamer (or hexamer) sequences total 1024 (or 4096) samples, a manageable size for a presynthesized library. This approach can replace the synthesis of ***primers*** , which is the current bottleneck in time and cost of the ***primer*** walking sequencing, and can allow full automation of the closed cycle of walking.

CONTROLLED TERM:
*Base Sequence
DNA: CH, chemistry
*DNA: GE, genetics
DNA, Viral: CH, chemistry
DNA, Viral: GE, genetics
*Databases, Factual
Molecular Sequence Data
***Oligodeoxyribonucleotides**
Oligodeoxyribonucleotides: CS, chemical synthesis
Templates

CAS REGISTRY NO.: 9007-49-2 (DNA)
CHEMICAL NAME: 0 (DNA, Viral); 0 (**Oligodeoxyribonucleotides**)

L5 ANSWER 34 OF 59 MEDLINE DUPLICATE 14
ACCESSION NUMBER: 93249449 MEDLINE
DOCUMENT NUMBER: 93249449 PubMed ID: 8387288
TITLE: Delineation of a DNA recognition element for the vitamin D3 receptor by binding site selection.
AUTHOR: Perez-Fernandez R; Arce V; Freedman L P
CORPORATE SOURCE: Dept. of Physiology, University of Santiago School of Medicine, Santiago de Compostela, Spain.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1993 Apr 30) 192 (2) 728-37.
Journal code: 9Y8; 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199306
ENTRY DATE: Entered STN: 19930618
Last Updated on STN: 19930618
Entered Medline: 19930601

ABSTRACT:
The vitamin D3 receptor is a ligand-inducible transcriptional regulatory protein. The receptor modulates the transcription of target genes by binding directly to specific DNA sites, termed vitamin D response elements; these sites vary considerably in their homologies to **each other**. In order to approach the question of what sequences can constitute high affinity recognition elements for the vitamin D3 receptor, we have selected for such sites in vitro by mixing overexpressed and purified vitamin D3 receptor DNA binding domain with an **oligonucleotide** duplex pool containing a completely randomized central region flanked by **primer-** ***annealing*** sites. Following multiple rounds of immunoprecipitation and amplification by PCR to enrich for high affinity sites, individual clones were sequenced and found to contain nearly identical hexameric sequences, yielding a consensus 5'-AGGGGG-3'. This sequence is similar to some known vitamin D3 receptor binding sites, such as osteocalcin, but quite divergent from others. This suggests that the vitamin D3 receptor may be able to selectively recognize at least two classes of sequence elements.

CONTROLLED TERM: Check Tags: Animal; Human; Support, Non-U.S. Gov't
Antibodies: IM, immunology
Base Sequence
Binding Sites
*Cholecalciferol: ME, metabolism
Cloning, Molecular
*DNA: ME, metabolism
Molecular Sequence Data
Receptors, Calcitriol
Receptors, Steroid: GE, genetics
Receptors, Steroid: IM, immunology
*Receptors, Steroid: ME, metabolism
Sequence Alignment
CAS REGISTRY NO.: 67-97-0 (Cholecalciferol); 9007-49-2 (DNA)
CHEMICAL NAME: 0 (Antibodies); 0 (Receptors, Calcitriol); 0 (Receptors, Steroid)

L5 ANSWER 35 OF 59 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 15
ACCESSION NUMBER: 1993:279115 BIOSIS
DOCUMENT NUMBER: PREV199396009340
TITLE: Analysis of Cochliobolus carbonum races by PCR amplification with arbitrary and gene-specific **primers**.
AUTHOR(S): Jones, Margaret J. (1); Dunkle, Larry D.
CORPORATE SOURCE: (1) U.S. Dep. Agric., Agric. Res. Serv., Purdue Univ., West Lafayette, IN 47907-1155 USA
SOURCE: Phytopathology, (1993) Vol. 83, No. 4, pp. 366-370. ISSN: 0031-949X.
DOCUMENT TYPE: Article
LANGUAGE: English
ABSTRACT:
The pathogenic races of Cochliobolus carbonum cause necrotic lesions of characteristic sizes and shapes on maize (Zea mays) leaves. To distinguish the races at the molecular level, isolates of C. carbonum races as well as other related species were analyzed by PCR (polymerase chain reaction) amplification of genomic DNA using either arbitrary **oligonucleotide primers** or **primers** with homology to sequences within the Tox2 locus, which is essential for production of a host-specific toxin. Amplification products from isolates of the four pathogenic races of C. carbonum were very similar to ***each*** **other** and to those from species thought to be closely related but were substantially different from nonpathogenic race 0 and from most other species. One of the arbitrary **primers** tested distinguished isolates of C. carbonum race 3 by the absence of two amplification products present in the other pathogenic races. The patterns of amplification products from races 2 and 4 were indistinguishable with the **primers** tested, suggesting that the recently described race 4 is not substantially different from race 2. **Primers** from the Tox2 locus distinguished race 1 isolates from isolates of other races. Only isolates of race 1 contained a single amplification product of the expected length when these **primers** were used under stringent **annealing** conditions. The results indicate that PCR amplification with arbitrary **primers** or gene-specific ***primers*** is useful for differentiating the races of C. carbonum and for examining their origins.
CONCEPT CODE: Genetics and Cytogenetics - Plant *03504
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biophysics - Molecular Properties and Macromolecules *10506
Agronomy - Grain Crops *52504
Phytopathology - Diseases Caused by Fungi *54502
BIOSYSTEMATIC CODE: Ascomycetes 15100
Gramineae *25305
INDEX TERMS: Major Concepts

Agronomy (Agriculture); Biochemistry and Molecular Biophysics; Genetics; Infection

INDEX TERMS: Industry
crop industry

INDEX TERMS: Miscellaneous Descriptors
AGRICULTURE; GENOMIC DNA; POLYMERASE CHAIN REACTION; RACE DIFFERENTIATION

ORGANISM: Super Taxa
Ascomycetes: Fungi, Plantae; Fungi - Unspecified: Fungi, Plantae; Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae; Plantae - Unspecified: Plantae

ORGANISM: Organism Name
fungus (Fungi - Unspecified); plant (Plantae - Unspecified); Cochliobolus carbonum (Ascomycetes); Zea mays (Gramineae)

ORGANISM: Organism Superterms
angiosperms; fungi; microorganisms; monocots; nonvascular plants; plants; spermatophytes; vascular plants

L5 ANSWER 36 OF 59 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
ACCESSION NUMBER: 1994-05476 BIOTECHDS
TITLE: Walking **primers** assembled from hexamers or pentamers;
hexamer and pentamer **oligonucleotide** DNA **primer** module application in DNA sequencing
(conference abstract)
AUTHOR: Kotler L; Zevin-Sonkin D; Sobolev I; Beskin A; Ulanovsky L
CORPORATE SOURCE: Weizmann-Inst.Sci.
LOCATION: Department of Structural Biology, Weizmann Institute of Science, Rehovot 76100, Israel.
SOURCE: Genome Mapping and Sequencing; (1993) 95
CODEN: 9999S
DOCUMENT TYPE: Journal
LANGUAGE: English
ABSTRACT: A striking effect displayed by 'modular **primers**', which consist of hexamer or pentamer **oligonucleotide** modules base-stacked to **each other** upon **annealing** to a DNA template, is reported. Such a combination of modules primed DNA sequencing reactions unlike either of the modules alone. This effect was attributed in part to the increase in the affinity of an **oligonucleotide** for the template in the presence of an adjacent module. All possible pentamer (or hexamer) sequences totaled 1024 (or 4096) samples, a manageable size for a presynthesized library. Unique priming could be achieved with modular **primers** with no ligation. Modular **primers** with Pu-Pu base-stacking between the 1st 2 hexamers showed a 91% success rate in sequencing reactions. This rate was comparable to the performance of conventional 17-mer **primers**. With processive sequencing of continuous DNA templates as long as tens of kb at hand, subcloning artefacts, such as DNA rearrangements, and unclonable segments would be minimized. (0 ref)
CLASSIFICATION: A GENETIC ENGINEERING AND FERMENTATION; A1 Nucleic Acid Technology
CONTROLLED TERMS: HEXAMER, PENTAMER **OLIGONUCLEOTIDE** DNA **PRIMER** MODULE, APPL. DNA SEQUENCING VOL.13, NO.10)

L5 ANSWER 37 OF 59 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
ACCESSION NUMBER: 1992-09010 BIOTECHDS
TITLE: Preparation of chimeric humanized antibody;
mouse complementarity determining region grafting method using the polymerase chain reaction and splicing by overlap extension for use in antibody engineering

RMS difference between the calculated and target interproton distance restraints is 0.033 .ANG., and the average atomic RMS differences between the 20 structures and their geometric average are 1.23 .ANG. for backbone atoms and 1.73 .ANG. for all heavy atoms. The dominating structural feature of the protein is a well-defined four-stranded antiparallel .beta.-sheet, two parallel .beta.-sheets packed antiparallel to **each other** and four short .alpha.- helices. The binding site of barwin to the tetramer N-acetylglucosamine has been qualitatively investigated, and the dissociation constant of the complex has been determined using one-dimensional 1H nuclear magnetic resonance spectroscopy.

CONTROLLED TERM: Medical Descriptors:
*amino terminal sequence
*carboxy terminal sequence
*protein secondary structure
*proton nuclear magnetic resonance
article
barley
binding site
calculation
computer program
hydrogen bond
nonhuman
nuclear overhauser effect
priority journal
protein domain
stereochemistry
stereospecificity
Drug Descriptors:
*basic protein: EC, endogenous compound
disulfide
n acetylglucosamine
oligosaccharide
vegetable protein: EC, endogenous compound

CAS REGISTRY NO.: (disulfide) 16734-12-6; (n acetylglucosamine) 7512-17-6

L5 ANSWER 39 OF 59 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
ACCESSION NUMBER: 1992-14336 BIOTECHDS
TITLE: Construction of a diverse Fab expression library from autoimmunized mice based on an improved preparation of cloning arms from bacteriophage vectors: a new library with potential for screening of biocatalysts;
Fab bank construction for use in catalytic antibody screening
AUTHOR: Shen G J; Wong C H
LOCATION: Department of Chemistry, The Scripps Research Institute, 10666 North Torrey Pines Road, La Jolla, CA 92037, USA.
SOURCE: Biocatalysis; (1992) 6, 2, 101-14
CODEN: BIOCED
DOCUMENT TYPE: Journal
LANGUAGE: English
ABSTRACT: A method for the construction in phage lambda of Fab cDNA expression libraries from autoimmunized mice that contain sufficiently diverse Fab fragments involves the use of **primer**-directed polymerase chain reaction amplification of total RNA from autoimmunized mice. The cloning arms used for the library construction were prepared from vectors Lc1 and Hc2. **Annealing**, dialysis and dephosphorylation after restriction enzyme cleavage of the vectors were critical for the efficient preparation of the cloning arms. The first heavy and light chain recombinatorial library constructed from autoimmunized mice was composed of about 5 million (BW heavy chain with (NZB x W)F1 light chain) and 2 million (BW heavy chain and BW light

Division, Los Alamos National Laboratory, Los Alamos, NM 87545, USA.
SOURCE: Abstr.Gen.Meet.Am.Soc.Microbiol.; (1991) 91 Meet., 302
DOCUMENT TYPE: Journal
LANGUAGE: English
ABSTRACT: Soil microorganisms which contain dioxygenase genes may be capable of in situ bioremediation of aromatic compounds. 2 Sets of polymerase chain reaction **primers**, with high homology for the ends of the xylE and nahH dioxygenase genes, were tested against genomic and plasmid DNA from Pseudomonas putida mt-2, P. putida G7 and Escherichia coli BHB2600. E. coli contained a todE dioxygenase gene on an inserted plasmid. XylE and nahH genes exhibited 80% homology with **each other** but only 20-23% homology with the todE gene. 30-Mer probes amplified only 1 DNA (940 bp) in mt-2 and G7 extracts and no DNA in E. coli. 20-Mer and 24-Mer **primers** amplified xylE and nahH in mt-2 and G7 respectively, and 4 additional DNAs in E. coli. E. coli amplified DNA exhibited low homology for xylE and high homology with the short 20- and 23-mer **primers** in Southern blots. Using these short **primers**, a higher **annealing** temp. of 65 deg was required to eliminate non-specific priming. The polymerase chain reaction was useful in screening DNA extracts for the presence of dioxygenase genes. (0 ref)
CLASSIFICATION: A MICROBIOLOGY; A1 Genetics; K BIOCATALYSIS; K1 Isolation and Characterization; M WASTE DISPOSAL; M1 Industrial Waste Disposal
CONTROLLED TERMS: DIOXYGENASE GENE E.G. XYLE, TODE, NAHH DETECTION IN PSEUDOMONAS PUTIDA, ESCHERICHIA COLI, POLYMERASE CHAIN REACTION, POT. APPL. IN BIOREMEDIATION, SOIL DECONTAMINATION BACTERIUM ENZYME POLLUTANT DEGRADATION WASTE-DISPOSAL

L5 ANSWER 42 OF 59 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1993:1640 CAPLUS
DOCUMENT NUMBER: 118:1640
TITLE: Analysis of H-ras oncogene mutations in bladder carcinoma tissue DNA by allele-specific polymerase chain reaction
AUTHOR(S): Klett, C.; Zuegel, M.; Becker, A.; Kruse-Jarres, J. D.
CORPORATE SOURCE: Inst. Klin. Chem., Katharinenhosp. Stuttgart, 7000/1, Germany
SOURCE: Adv. Mol. Genet. (1991), 3(Mol. Biol. Tumour Res.), 29-38
CODEN: AMGEEU
DOCUMENT TYPE: Journal
LANGUAGE: English
CLASSIFICATION: 3-1 (Biochemical Genetics)
ABSTRACT:
A rapid nonradioactive method is described to detect point mutations in the H-ras oncogene in bladder carcinoma tissue based on allele-specific polymerase chain reaction (ASPCR). This method allows direct detection of the normal or mutant H-ras oncogene allele in genomic DNA. The PCR product could be visualized directly after electrophoresis in ethidium bromide-stained agarose gels under UV-light. Addnl. steps as Southern blotting, probe hybridization, or restriction enzyme cleavage are now unecessary. In ASPCR, two allele-specific **oligonucleotide primers**, one specific for the mutant H-ras allele (Codon 12: GTC) and one specific for the normal H-ras allele (Codon 12: GGC), together with another **primer** complementary to both alleles were used in the polymerase chain reaction with genomic templates. The allele-specific **primers** only differed from **each** ***other*** in their terminal 3' nucleotide (T or G). Under optimized conditions of PCR and **annealing** temp. these **primers** only directed amplification on their complementary allele. In this study, the

authors detected in bladder carcinoma tissues of 29 patients one patient contg. a H-ras codon 12 point mutation (G - T).

SUPPL. TERM: gene Nras mutation bladder carcinoma PCR; human bladder carcinoma gene Nras mutation
INDEX TERM: Polymerase chain reaction
(allele-specific, human gene N-ras mutations detected by, in bladder carcinoma)
INDEX TERM: Mutation
(in gene N-ras, in human bladder carcinoma, detection by allele-specific PCR of)
INDEX TERM: Bladder
(neoplasm, carcinoma, of human, gene N-ras mutations detection in, allele-specific PCR for)
INDEX TERM: Gene, animal
ROLE: BIOL (Biological study)
(N-ras, in human bladder carcinoma, mutation in, detection by allele-specific PCR of)

L5 ANSWER 43 OF 59 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 17
ACCESSION NUMBER: 1992:450931 BIOSIS
DOCUMENT NUMBER: BA94:92331
TITLE: SITE-SPECIFIC MUTAGENESIS AND DNA RECOMBINATION BY USING PCR TO GENERATE RECOMBINANT CIRCLES IN-VITRO OR BY RECOMBINATION OF LINEAR PCR PRODUCTS IN-VIVO.
AUTHOR(S): JONES D H; WINISTORFER S C
CORPORATE SOURCE: DEP. PEDIATR., COLL. MED., UNIV. IOWA, IOWA CITY, IOWA 52242.
SOURCE: METHODS (ORLANDO), (1991) 2 (1), 2-10.
CODEN: MTHDE9. ISSN: 1046-2023.
FILE SEGMENT: BA; OLD
LANGUAGE: English
ABSTRACT:
This article describes two methods in which the polymerase chain reaction (PCR) is used for site-specific mutagenesis and for DNA recombination without any enzymatic reaction in vitro apart from DNA amplification. The first method generates DNA joints in vitro by using separate PCR amplification to generate products that when combined, denatured, and reannealed form double-stranded DNA with single-stranded ends. These single-stranded ends are designed to ***anneal*** to **each other** to yield circles, an application termed recombinant circle PCR (RCPCR). RCPCR-generated DNA circles form without restriction enzyme digestion or ligation and can be transfected directly into Escherichia coli. The second method generated DNA joints in vivo by using the polymerase chain reaction to add homologous ends to DNA. Following transfection of the linear PCR product(s) into strains of E. coli used routinely in cloning, recombination of these homologous ends in vivo permits cloning of the mutant or recombinant of interest. The second method, termed recombination PCR (RPCR), diminished the number of **primers** necessary to generate a given mutant or recombinant to half that necessary in RCPCR, because it eliminates the need to generate staggered ends in vitro.
CONCEPT CODE: Cytology and Cytochemistry - Animal *02506
Genetics and Cytogenetics - Animal *03506
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Enzymes - Methods *10804
Physiology and Biochemistry of Bacteria *31000
Genetics of Bacteria and Viruses *31500
In Vitro Studies, Cellular and Subcellular 32600
BIOSYSTEMATIC CODE: Enterobacteriaceae 06702
INDEX TERMS: Miscellaneous Descriptors

ESCHERICHIA-COLI POLYMERASE CHAIN REACTION

L5 ANSWER 44 OF 59 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
ACCESSION NUMBER: 1990-14558 BIOTECHDS
TITLE: DNA amplification;
for genome DNA sequencing by **annealing** of DNA **primer** and incubation with phage T7 DNA-polymerase having reduced exonuclease activity; DNA sequence
PATENT ASSIGNEE: Harvard-College
PATENT INFO: EP 386857 12 Sep 1990
APPLICATION INFO: EP 1987-201138 24 Dec 1987
PRIORITY INFO: US 1987-132569 14 Dec 1987; US 1987-3227 14 Jan 1987
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1990-276890 [37]
ABSTRACT: A method of amplification of a DNA sequence comprises: (a) **annealing** a first and second **primer** to opposite strands of a double-stranded DNA sequence so that the **primers'** 3' ends are directed toward **each other**; and (b) incubating the **annealed** mixture with a DNA-polymerase (EC-2.7.7.7) obtained from phage T7 but having less than 50%, and preferably less than 1%, of the exonuclease activity of the naturally associated level of exonuclease activity of the enzyme. The DNA-polymerase may be obtained by chemically modifying the natural enzyme or by mutagenesis of the coding region of the gene encoding exonuclease activity. The DNA-polymerase can synthesize through regions of secondary structure resulting in longer extensions. It is possible to amplify a specific region of the human genomic DNA over 200,000 times. This facilitates both the cloning and direct analysis of genomic DNA. The DNA-polymerase is suitable for DNA sequencing. (43pp)
CLASSIFICATION: A MICROBIOLOGY; A1 Genetics; K BIOCATALYSIS; K1 Isolation and Characterization
CONTROLLED TERMS: PHAGE T7 DNA-POLYMERASE MUTAGENESIS, DNA SEQUENCE, ENZYME ENGINEERING, REDUCED EXONUCLEASE ACT., APPL. DNA AMPLIFICATION, POT. HUMAN GENOME DNA SEQUENCING MAMMAL EC-2.7.7.7 PROTEIN ENGINEERING

L5 ANSWER 45 OF 59 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1990:515717 CAPLUS
DOCUMENT NUMBER: 113:115717
TITLE: Physical properties of glycosyl diacylglycerols. 1. Calorimetric studies of a homologous series of 1,2-di-O-acyl-3-O-(.alpha.-D-glucopyranosyl)-sn-glycerols
AUTHOR(S): Mannock, David A.; Lewis, Ruthven N. A. H.; McElhaney, Ronald N.
CORPORATE SOURCE: Dep. Biochem., Univ. Alberta, Edmonton, AB, T6G 2H7, Can.
SOURCE: Biochemistry (1990), 29(34), 7790-9
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English
CLASSIFICATION: 33-4 (Carbohydrates)
Section cross-reference(s): 6, 22, 68
ABSTRACT:
The polymorphic phase behavior of aq. dispersions of a homologous series of 1,2-.omega.-acyl-3-O-(.alpha.-D-glucopyranosyl)-sn-glycerols was studied by differential scanning calorimetry. At fast heating rates unannealed samples of these lipids exhibit a strongly energetic transition, which was identified as a lamellar gel/liq. cryst. (L.beta./L.alpha.) phase transition (short- and medium-chain compds.) or a lamellar gel to inverted hexagonal

(L.beta./HII)phase transition (long-chain compds.) by X-ray diffraction studies (Sen et al., 1990). At still higher temps., some of the lipids that form lamellar liq.-cryst. phases exhibit an addnl. transition, which as identified as a transition to an inverted nonbilayer phase by X-ray diffraction studies. The lamellar gel phase formed on initial cooling of these lipids is a metastable structure, which, when **annealed** under appropriate conditions, transforms to a more stable lamellar gel phase, which was identified as a poorly hydrated crystallike phase with tilted acyl chains by x-ray diffraction measurements (Se, et al, 1990). With the exception of the di-19:0 homolog the cryst. phases of these lipids are stable to temps. higher than those at which their L.beta. phases melt and, as a result, they convert directly to L.alpha. or HII phases on heating. The results indicate that the length of the acyl chain affects both the kinetic and thermodn. properties of the cryst. phases of these lipids as well as the type of nonbilayer phase that they form. Moreover, when compared with the .beta.-anomers, these .alpha.-D-glucosyl diacylglycerols are more prone to form ordered cryst. gel phases at low temps. and are somewhat less prone to form nonbilayer phases at elevated temps. Thus the phys. properties of glucolipids (and possibly all glycolipids) are very sensitive to the nature of the anomeric linkage between the sugar headgroup and the glycerol backbone of the lipid mol. It was suggested that this is, in part, due to a change in orientation of the glucopyranosyl ring relative to the bilayer surface, which in turn affects the way(s) in which the sugar head groups interact with **each** ***other*** and with water.

SUPPL. TERM: glycosyldiacylglycerol phys property calorimetry thermodn; glycerol glycosyldiacyl phys property calorimetry thermodn; phase transition glycosyldiacyl glycerol; glycolipid phys property calorimetry thermodn; polymorphism glycosyldiacylglycerol

INDEX TERM: Glycolipids
ROLE: RCT (Reactant)
(glycosyl diacylglycerols, polymorphic phase behavior of, calorimetric study of)

INDEX TERM: Phase transition
Physical property
Thermodynamics
(of glycosyl diacylglycerols, calorimetric study of)

INDEX TERM: Entropy
(of phase transition of glycosyl diacylglycerols)

INDEX TERM: Conformation and Conformers
(anomeric effect, of glycosyl diacylglycerols)

INDEX TERM: **Oligosaccharides**
ROLE: RCT (Reactant)
(di-, diglycosyldiacylglycerols, polymorphic phase behavior of, calorimetric study of)

INDEX TERM: Calorimetry
(differential scanning, study of polymorphic phase behavior of glycosyl diacylglycerols)

INDEX TERM: 65529-92-2 66429-10-5 128903-05-9 128903-06-0 128903-07-1 128903-08-2 128903-09-3 128903-10-6 128903-11-7 128923-50-2 128949-00-8
ROLE: RCT (Reactant)
(polymorphic phase behavior of, calorimetric study of)

L5 ANSWER 46 OF 59 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 90278110 MEDLINE
DOCUMENT NUMBER: 90278110 PubMed ID: 2191042
TITLE: Technical aspects of typing for HLA-DP alleles using allele-specific DNA in vitro amplification and sequence-specific **oligonucleotide** probes. Detection of single base mismatches.
AUTHOR: Fugger L; Morling N; Ryder L P; Odum N; Svejgaard A
CORPORATE SOURCE: Department of Clinical Immunology, State University

Hospital, Copenhagen, Denmark.
SOURCE: JOURNAL OF IMMUNOLOGICAL METHODS, (1990 May 25) 129 (2) 175-85.
Journal code: IFE; 1305440. ISSN: 0022-1759.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199007
ENTRY DATE: Entered STN: 19900824
Last Updated on STN: 19900824
Entered Medline: 19900717

ABSTRACT:
The polymerase chain reaction (PCR) is an effective method for in vitro DNA amplification which combined with probing with synthetic ***oligonucleotides*** can be used for, e.g., HLA-typing. We have studied the technical aspects of HLA-DP typing with the technique. DNA from mononuclear nucleated cells was extracted with either a simple salting out method or phenol/chloroform. Both DNAs could be readily used for PCR. The MgC2 concentration of the PCR buffer and the **annealing** temperature of the thermal cycle of the PCR were the two most important variables. The MgCl2 concentration and the temperature must be carefully titrated for each ***primer*** pair in the PCR. The influence of mismatches between the ***primer*** and the DNA template were studied and we found that, by using ***primers*** differing only from **each other** at the 3' end, cross-amplification of closely homologous alleles could be avoided. Thus, single base mismatches may be detected in the PCR and typing for HLA-DP gene variants, which differ for only one base, may be performed.

CONTROLLED TERM: Check Tags: Human; Support, Non-U.S. Gov't
Alleles
Amino Acid Sequence
Base Sequence
DNA Probes, HLA
Genetic Techniques
*HLA-DP Antigens: GE, genetics
Magnesium Chloride
Molecular Sequence Data
Nucleic Acid Hybridization
Polymerase Chain Reaction
Temperature
Variation (Genetics)
CAS REGISTRY NO.: 7786-30-3 (Magnesium Chloride)
CHEMICAL NAME: 0 (DNA Probes, HLA); 0 (HLA-DP Antigens)

L5 ANSWER 47 OF 59 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1990:568501 CAPLUS
DOCUMENT NUMBER: 113:168501
TITLE: Method and reagents for detecting nucleic acid sequences
INVENTOR(S): Richards, Rodney M.; Jones, Theodore
PATENT ASSIGNEE(S): Amgen, Inc., USA
SOURCE: PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
INT. PATENT CLASSIF.:
MAIN: C12Q001-68
SECONDARY: G01N033-48
CLASSIFICATION: 9-2 (Biochemical Methods)
Section cross-reference(s): 33
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 8912696	A1	19891228	WO 1989-US2649	19890616
W: AU, JP				
RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
AU 8938601	A1	19900112	AU 1989-38601	19890616
AU 634969	B2	19930311		
EP 379559	A1	19900801	EP 1989-907963	19890616
EP 379559	B1	19961023		
R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
JP 03501211	T2	19910322	JP 1989-507372	19890616
JP 2801051	B2	19980921		
AT 144556	E	19961115	AT 1989-907963	19890616
JP 10309195	A2	19981124	JP 1998-45804	19890616
CA 1340160	A1	19981208	CA 1989-603916	19890626
PRIORITY APPLN. INFO.:			US 1988-220108	19880624
			JP 1989-507372	19890616
			WO 1989-US2649	19890616

ABSTRACT:
A method for detecting a target nucleic acid sequence optionally employing both an amplification procedure and a detection procedure is disclosed. Amplification is accomplished through the use of plurality of pairs of nucleic acid amplification probes, wherein the member probes of each pair of amplification probes are complementary to **each other**, with .gtoreq.1 hybridizing member of each pair of amplification probes also being complementary to a given portion of the target nucleic acid sequence, which acts as a template. The hybridizing members of each pair of amplification probes hybridize to the target sequence in a continuous manner, sufficiently adjacent to **each other** to enable the probes to be joined together to form an amplification product. Once the hybridizing amplification probes are joined, the completed amplification product can be sepd. by denaturation, and the process repeated, until a sufficient quantity of the target nucleic acid sequence is produced to result in measurable signal in the selected assay. The correctly assembled amplification product serves as a template in a manner similar to that served by the target nucleic acid sequence in the amplification procedure. Thus, target sequence 5'-GATAAGGAGGATTTGATGGGAGAGGTTAATTATTGGCAGGGGAGG-3' (synthetic ***oligonucleotide*** of Pst1 fragment of human T-lymphotropic virus-1) was mixed with detection probes 5'-GCCAATAATTAACCT-3' and phosphorylated 5'-CTCCCATCAAATCCT-3', heated at 90.degree. for 5 min, and **annealed** at room temp. for 15 min. Ligation then proceeded for 5 min at room temp, the reaction was quenched with EDTA/dye, and the mixt. was heated at 90.degree. for 5 min with subsequent quick chilling on ice. The expected 30-mer detection product was found. Synthesis of probes is described.

SUPPL. TERM: nucleic acid hybridization amplification; human lymphotropic virus detection DNA hybridization

INDEX TERM: Deoxyribonucleic acid formation
(amplification, in nucleic acid hybridization)

INDEX TERM: Nucleic acid hybridization
(multiple amplification and detection probes in)

INDEX TERM: Virus, animal
(human T-cell leukemia type I, PstI fragment of, synthetic **oligonucleotides** of, as amplification and detection probes for nucleic acid hybridization)

INDEX TERM: 9080-13-1, Ligase
ROLE: ANST (Analytical study)
(in nucleic acid hybridization)

INDEX TERM: 129923-38-2P 129923-39-3P 129923-55-3P 129923-56-4P
ROLE: SPN (Synthetic preparation); PREP (Preparation)
(prepn. of amplification and target sequence, of PstI fragment of human T-lymphotropic virus-1, for nucleic acid hybridization)

INDEX TERM: 129923-12-2P 129923-14-4P 129923-15-5P 129923-17-7P

([Leu-17]vasoactive intestinal polypeptide analog gene on)

INDEX TERM: Escherichia coli
(cloning and expression in, of [Leu-17]vasoactive intestinal polypeptide analog genes)

INDEX TERM: Gene and Genetic element, animal
ROLE: PREP (Preparation)
(for [Leu-17]vasoactive intestinal polypeptide analogs, simultaneous prepn.of, expression in Escherichia coli of)

INDEX TERM: Molecular cloning
(of [Leu-17]vasoactive intestinal polypeptide analog genes, in Escherichia coli)

INDEX TERM: Protein sequences
(of [Leu-17]vasoactive intestinal polypeptide analogs of human, complete)

INDEX TERM:

126467-65-0	126467-66-1	126467-67-2	126467-68-3
126467-69-4	126467-70-7	126467-71-8	126467-72-9
126467-73-0	126467-74-1	126467-75-2	126467-76-3
126467-77-4	126467-78-5	126467-79-6	126467-80-9
126467-81-0	126529-32-6	126529-33-7	126529-34-8
126529-35-9	126529-36-0	126529-37-1	126529-38-2
126529-39-3	126529-40-6	126529-41-7	126529-42-8
126529-43-9	126529-44-0	126529-45-1	126529-46-2
126529-47-3	126529-48-4	126529-49-5	126529-50-8
126529-51-9	126529-52-0	126529-53-1	126529-54-2
126529-55-3	126553-52-4	126553-53-5	126553-54-6
126553-55-7	126553-56-8		

ROLE: PRP (Properties)
([Leu-17]vasoactive intestinal polypeptide analog, gene for, synthesis and expression in Escherichia coli of)

INDEX TERM: 37221-79-7P, Vasoactive intestinal polypeptide
ROLE: PREP (Preparation)
(analogs of, genes for, simultaneous prepn. of, expression in Escherichia coli of)

L5 ANSWER 49 OF 59 MEDLINE DUPLICATE 19
ACCESSION NUMBER: 89202405 MEDLINE
DOCUMENT NUMBER: 89202405 PubMed ID: 2704745
TITLE: Allele-specific enzymatic amplification of beta-globin genomic DNA for diagnosis of sickle cell anemia.
AUTHOR: Wu D Y; Ugozzoli L; Pal B K; Wallace R B
CORPORATE SOURCE: Department of Molecular Biochemistry, Beckman Research Institute of the City of Hope, Duarte, CA 91010.
CONTRACT NUMBER: CA33572 (NCI)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1989 Apr) 86 (8) 2757-60.
Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198905
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 19970203
Entered Medline: 19890524

ABSTRACT:
A rapid nonradioactive approach to the diagnosis of sickle cell anemia is described based on an allele-specific polymerase chain reaction (ASPCR). This method allows direct detection of the normal or the sickle cell beta-globin allele in genomic DNA without additional steps of probe hybridization, ligation, or restriction enzyme cleavage. Two allele-specific ***oligonucleotide*** **primers**, one specific for the sickle cell allele and one specific for the normal allele, together with another ***primer*** complementary to both alleles were used in the polymerase chain

reaction with genomic DNA templates. The allele-specific **primers** differed from **each other** in their terminal 3' nucleotide. Under the proper **annealing** temperature and polymerase chain reaction conditions, these **primers** only directed amplification on their complementary allele. In a single blind study of DNA samples from 12 individuals, this method correctly and unambiguously allowed for the determination of the genotypes with no false negatives or positives. If ASPCR is able to discriminate all allelic variation (both transition and transversion mutations), this method has the potential to be a powerful approach for genetic disease diagnosis, carrier screening, HLA typing, human gene mapping, forensics, and paternity testing.

CONTROLLED TERM: Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
Alleles
*Anemia, Sickle Cell: DI, diagnosis
Fluorescent Dyes
*Gene Amplification
*Globins: GE, genetics
Oligonucleotide Probes
CAS REGISTRY NO.: 9004-22-2 (Globins)
CHEMICAL NAME: 0 (Fluorescent Dyes); 0 (**Oligonucleotide** Probes)

L5 ANSWER 50 OF 59 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1989:3061 CAPLUS
DOCUMENT NUMBER: 110:3061
TITLE: Sequence dependence of DNA structure. The B, Z, and A conformations of polydeoxynucleotides containing repeating units of 6 to 16 base pairs
AUTHOR(S): Luthman, Kristina; Behe, Michael J.
CORPORATE SOURCE: Dep. Chem., Lehigh Univ., Bethlehem, PA, 18015, USA
SOURCE: J. Biol. Chem. (1988), 263(30), 15535-9
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
CLASSIFICATION: 6-2 (General Biochemistry)
ABSTRACT:
In order to study the sequence dependence of the B-Z transition, 8 double-stranded polydeoxynucleotides were synthesized. The polymers have been defined, alternating purine-pyrimidine sequences with repeating units of 6-16 base pairs, and contain 12.5-33% AT base pairs, and contain 12.5-33% AT base pairs. Adenine and thymine nucleotides are in nearest-neighbor positions in the series poly[d[TA(CG)2-7]], but are isolated from **each** ***other*** , with min. sepns. of 2 and 6 GC base pairs, in poly[d[TGCA(CG)6]] and poly[T(GC)3A(CG)4)]], resp. All of the polymers except poly[d[TA(CG)2]] were shown by CD to undergo a right- to left-hand helical transition at high NaCl concns., and all polymers exhibited a B to A transition in the presence of EtOH. Poly[d[TA(CG)7]] was the only polymer to undergo a B to Z to A transition in EtOH. At a const. percentage of AT base pairs, the B-Z transition is sequence-dependent, occurring at lower salt concns. for polymers contg. longer runs of contiguous GC base pairs in the repeating unit.

SUPPL. TERM: DNA conformation sequence; polydeoxynucleotide conformation sequence
INDEX TERM: Deoxyribonucleic acids
ROLE: PRP (Properties)
(conformation of, sequence dependence of)
INDEX TERM: Conformation and Conformers
(of DNA, sequence dependence of)
INDEX TERM: Ionic strength
(sequence-dependent conformational transitions of **oligodeoxyribonucleotides** response to)
INDEX TERM: Free energy
(conformational, of **oligodeoxyribonucleotides**,

sequence dependence of)

INDEX TERM: Nucleotides, polymers
ROLE: SPN (Synthetic preparation); PREP (Preparation)
(**oligo**-, deoxyribo-, prepn. and sequence-dependent conformational transitions of double-stranded)

INDEX TERM: 117695-41-7P 117695-43-9P 117695-45-1P 117714-94-0P
117787-58-3P 117787-59-4P 117787-60-7P 117846-54-5P
ROLE: SPN (Synthetic preparation); PREP (Preparation)
(double-stranded, prepn. and sequence-dependent conformational transitions of)

INDEX TERM: 36786-90-0 117714-96-2
ROLE: BIOL (Biological study)
(double-stranded, sequence-dependent conformational transitions of)

INDEX TERM: 112430-35-0P 117697-63-9P 117697-74-2P 117697-75-3P
117697-76-4P 117820-48-1P 117820-49-2P 117852-34-3P
ROLE: SPN (Synthetic preparation); PREP (Preparation)
(prepn. and spontaneous **annealing** and ligation of)

INDEX TERM: 64-17-5, Ethanol, properties
ROLE: PRP (Properties)
(sequence-dependent conformational transitions of **oligodeoxyribonucleotides** response to)

L5 ANSWER 51 OF 59 MEDLINE DUPLICATE 20

ACCESSION NUMBER: 88321655 MEDLINE
DOCUMENT NUMBER: 88321655 PubMed ID: 3413476
TITLE: A ligase-mediated gene detection technique.
AUTHOR: Landegren U; Kaiser R; Sanders J; Hood L
CORPORATE SOURCE: Division of Biology, California Institute of Technology, Pasadena 91125.
SOURCE: SCIENCE, (1988 Aug 26) 241 (4869) 1077-80.
Journal code: UJ7; 0404511. ISSN: 0036-8075.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198809
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19980206
Entered Medline: 19880923

ABSTRACT:
An assay for the presence of given DNA sequences has been developed, based on the ability of two **oligonucleotides** to **anneal** immediately adjacent to **each other** on a complementary target DNA molecule. The two **oligonucleotides** are then joined covalently by the action of a DNA ligase, provided that the nucleotides at the junction are correctly base-paired. Thus single nucleotide substitutions can be distinguished. This strategy permits the rapid and standardized identification of single-copy gene sequences in genomic DNA.

CONTROLLED TERM: Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.
Amino Acid Sequence
Base Sequence
Cell Line
*DNA: AN, analysis
DNA: GE, genetics
DNA: ME, metabolism
*DNA Ligases: ME, metabolism
DNA, Recombinant: ME, metabolism
Fluorescent Dyes
Globins: GE, genetics

Molecular Sequence Data
Nucleic Acid Denaturation
Nucleic Acid Hybridization
Polymorphism (Genetics)
*Polynucleotide Ligases: ME, metabolism
CAS REGISTRY NO.: 9004-22-2 (Globins); 9007-49-2 (DNA)
CHEMICAL NAME: 0 (DNA, Recombinant); 0 (Fluorescent Dyes); EC 6.5.1. (Polynucleotide Ligases); EC 6.5.1.- (DNA Ligases)

L5 ANSWER 52 OF 59 MEDLINE
ACCESSION NUMBER: 88096656 MEDLINE
DOCUMENT NUMBER: 88096656 PubMed ID: 3697135
TITLE: Solid-phase assembly of DNA duplexes from synthetic **oligonucleotides**.
AUTHOR: Hostomsky Z; Smrt J
CORPORATE SOURCE: Institute of Molecular Genetics, Czechoslovak Academy of Sciences, Prague.
SOURCE: NUCLEIC ACIDS SYMPOSIUM SERIES, (1987) (18) 241-4. Journal code: O8N; 8007206. ISSN: 0261-3166.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198801
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19900305
Entered Medline: 19880127

ABSTRACT:
A new method of rapid and efficient assembly of extended DNA duplexes in solid phase was developed. Subassemblies of separately **annealed** ***oligonucleotides*** were stepwise hybridized to **each** ***other*** on a solid support. Two types of supports with anchor ***oligonucleotide*** were tested: Fractosil-1000 with **oligo**-dT sequence and Sephacryl S-500 with an **oligonucleotide** bound via CNBr-activation procedure. Sephacryl S-500 turned out to be the support of choice since all enzymatic reactions of the assembly procedure (phosphorylation, ligation, restriction enzyme digestion) could be efficiently performed with DNA immobilized on Sephacryl S-500 particles.

CONTROLLED TERM: Acrylic Resins
*DNA: CS, chemical synthesis
*Genes, Synthetic
Indicators and Reagents
***Oligodeoxyribonucleotides: CS, chemical synthesis**
Oligodeoxyribonucleotides: IP, isolation & purification
CAS REGISTRY NO.: 9007-49-2 (DNA)
CHEMICAL NAME: 0 (Acrylic Resins); 0 (Indicators and Reagents); 0 (**Oligodeoxyribonucleotides**); 0 (Sephacryl Superfine)

L5 ANSWER 53 OF 59 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1987:548577 CAPLUS
DOCUMENT NUMBER: 107:148577
TITLE: Solid-phase assembly of DNA duplexes from synthetic **oligonucleotides**
AUTHOR(S): Hostomsky, Zdenek; Smrt, Jiri
CORPORATE SOURCE: Inst. Mol. Genet., Czech. Acad. Sci., Prague, 166 37, Czech.
SOURCE: Nucleic Acids Symp. Ser. (1987), 18(Symp. Chem. Nucleic Acid Compon., 7th, 1987), 241-4
CODEN: NACSD8; ISSN: 0261-3166
DOCUMENT TYPE: Journal
LANGUAGE: English
CLASSIFICATION: 3-5 (Biochemical Genetics)

ABSTRACT:
A method for the rapid and efficient solid phase assembly of extended DNA duplexes was developed. Subassemblies of sep. **annealed** ***oligonucleotides*** were stepwise hybridized to **each** ***other*** on a solid support. Two types of supports with anchor ***oligonucleotides*** were tested: Fractosil-1000 with an **oligo**-dT sequence and Sephacryl S-500 with an **oligonucleotide** bound via CNBr-activation procedure. Sephacryl S-500 turned out to be the support of choice since all enzymic reactions of the assembly procedure (phosphorylation, ligation, restriction enzyme digestion) could be efficiently performed with DNA immobilized on Sephacryl S-500 particles.

SUPPL. TERM: DNA prepn solid phase **oligonucleotide**
INDEX TERM: Deoxyribonucleic acids
Gene and Genetic element
ROLE: PREP (Preparation)
(prepn. of, from synthetic **oligonucleotides**)
INDEX TERM: Nucleotides, polymers
ROLE: PREP (Preparation)
(**oligo-**, genetic, DNA prepn. from)
INDEX TERM: 84593-65-7, Sephacryl S-500
ROLE: PRP (Properties)
(DNA immobilization on, for DNA prepn. from synthetic **oligonucleotides**)

L5 ANSWER 54 OF 59 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1986:142988 CAPLUS
DOCUMENT NUMBER: 104:142988
TITLE: Molecular cloning and sequence analysis of Newcastle disease virus
AUTHOR(S): Chambers, Philip; Millar, Neil S.; Emmerson, Peter T.; Bingham, Richard W.
CORPORATE SOURCE: Dep. Biochem., Univ. Newcastle upon Tyne, Newcastle upon Tyne, NE1 7RU, UK
SOURCE: Biochem. Soc. Trans. (1986), 14(1), 100-1
CODEN: BCSTB5; ISSN: 0300-5127
DOCUMENT TYPE: Journal
LANGUAGE: English
CLASSIFICATION: 3-2 (Biochemical Genetics)
ABSTRACT:
Genomic RNA was isolated from egg-grown Newcastle disease virus (NDV) and cDNA prepd. using reverse transcriptase and a random hexanucleotide **primer**. The resulting RNA:DNA hybrids were tailed with **oligo**(dC) and ***annealed*** to plasmid pBR322. The **annealed** mixt. was transformed into Escherichia coli. NDV-specific recombinants were detected by colony hybridization, using 35S-labeled cDNA to virion RNA as a probe. Clones that hybridized strongly to the probe were characterized for insert size; the inserts were mapped resp. to **each other** by dot blot hybridization and restriction mapping. DNA sequence anal. of the C-terminal portion of the hemagglutinin-neuraminidase (HN) [9001-67-6] gene revealed an open reading frame that shows striking similarity to the same C-terminal sequence in the HN gene from SV5 virus. The entire HN and fusion protein genes were cloned into pBR322.

SUPPL. TERM: Newcastle disease virus cloning structure
INDEX TERM: Gene and Genetic element, microbial
ROLE: BIOL (Biological study)
(of Newcastle disease virus, cloning and structure of)
INDEX TERM: Ribonucleic acids, viral
ROLE: PROC (Process)
(of Newcastle disease virus, genomic organization of)
INDEX TERM: Molecular cloning
(of RNA, of Newcastle disease virus)
INDEX TERM: Virus, animal

(Newcastle disease, RNA of, cloning and structure of)
INDEX TERM: Agglutinins and Lectins
ROLE: PRP (Properties)
(hemagglutinins, gene for, of Newcastle disease virus, structure of)
INDEX TERM: 9001-67-6
ROLE: PRP (Properties)
(gene for, of Newcastle disease virus, structure of)

L5 ANSWER 55 OF 59 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 86062892 MEDLINE
DOCUMENT NUMBER: 86062892 PubMed ID: 2999421
TITLE: Sequence alterations in temperature-sensitive M-protein mutants (complementation group III) of vesicular stomatitis virus.
AUTHOR: Gopalakrishna Y; Lenard J
CONTRACT NUMBER: AI-13003 (NIAID)
SOURCE: JOURNAL OF VIROLOGY, (1985 Dec) 56 (3) 655-9.
Journal code: KCV; 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M11754
ENTRY MONTH: 198601
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19970203
Entered Medline: 19860102

ABSTRACT:
Sequences were determined of the coding regions of the M-protein genes of the Glasgow and Orsay strains of vesicular stomatitis virus (Indiana serotype) and of two group III (M-protein) mutants derived from each wild type. Synthetic ***primers*** were **annealed** with viral genomic RNA and extended with reverse transcriptase. The resulting high-molecular-weight cDNA was sequenced directly. Both Glasgow and Orsay wild types differed in 13 bases from a clone of the San Juan strain sequenced by J. K. Rose and C. J. Gallione (J. Virol. 39:519-528, 1981). Six of these base changes caused amino acid changes in each wild type, whereas seven were degenerate. The Orsay and Glasgow sequences resembled **each other** more closely than either resembled that of Rose and Gallione, differing in eight nucleotides and four amino acids. Each of the four mutants, however, differed from its parent wild type in only one or two point mutations. Every mutation caused a change either from or to a charged amino acid; the change for tsG31 was Lys (position 215) to Glu, the change for tsO23 was Gly (position 21) to Glu, the change for tsO89 was Ala (position 133) to Asp, the changes for tsG33 were Lys (position 204) to Thr and Glu (position 214) to Lys. The charge differences predicted from these amino acid changes was confirmed by nonequilibrium pH gradient electrophoresis for tsG31, tsG33, tsO23, and the two wild types. These mutations affect residues spanning nearly 85% of the linear sequence, although the mutants possess nearly identical phenotypic properties.

CONTROLLED TERM: Check Tags: Support, U.S. Gov't, P.H.S.
Amino Acid Sequence
Base Sequence
DNA: GE, genetics
Isoelectric Point
Mutation
Structure-Activity Relationship
Temperature
*Vesicular Stomatitis-Indiana Virus: GE, genetics
*Viral Proteins: GE, genetics
CAS REGISTRY NO.: 9007-49-2 (DNA)
CHEMICAL NAME: 0 (Viral Proteins)

(amino acid sequence of)
INDEX TERM: 83534-89-8
ROLE: PRP (Properties)
(amino acid sequences of)
INDEX TERM: 85255-81-8 90897-08-8
ROLE: PRP (Properties)
(nucleotide sequence of)

L5 ANSWER 58 OF 59 MEDLINE DUPLICATE 23
ACCESSION NUMBER: 81112142 MEDLINE
DOCUMENT NUMBER: 81112142 PubMed ID: 6893953
TITLE: Regulation of actin polymerization by villin, a 95,000 dalton cytoskeletal component of intestinal brush borders.
AUTHOR: Craig S W; Powell L D
SOURCE: CELL, (1980 Dec) 22 (3) 739-46.
Journal code: CQ4; 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198104
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19900316
Entered Medline: 19810413

ABSTRACT:
A 95,000 dalton actin-binding polypeptide, villin, has been purified to 98% homogeneity from brush border cytoskeletons of chicken intestinal epithelial cells. In vitro, this protein exerts control over the polymerization of actin. In the presence of villin, the lag phase preceding detectable actin polymerization is shortened and the steady state equilibrium viscosity is reduced in proportion to the amount of villin present. A molar ratio of villin:actin of 1:40 results in a 70% reduction of the Ostwald viscosity. Significant effects can be detected at a ratio of 1:600. These ratios are physiologically relevant because the ratio of villin:actin in brush borders is 1:13 and in isolated microvilli is 1:9-12. Reduction of viscosity is mirrored by an increase in the amount of protein which fails to sediment at 150,000 X g for 60 min. An assay of the nonsedimentable protein for actin monomers by the inhibition of DNAase I showed that the concentration of monomer was not significantly altered by the presence of villin. Electron microscopic examination of negatively stained, nonsedimentable actin demonstrated that the presence of villin during actin polymerization results in the production of short **oligomers** which cannot **anneal** with **each** ***other*** to form long filaments. Villin is also effective in reducing the viscosity of F-actin when it is added to a fuly polymerized actin sample. In view of these striking properties, villin is likely to be an important in vivo regulator of cytoskeletal structure and, by implication, of cell shape and motility.

CONTROLLED TERM: Check Tags: Animal; Support, U.S. Gov't, P.H.S.
*Actins: ME, metabolism
Carrier Proteins: IP, isolation & purification
*Carrier Proteins: ME, metabolism
*Cell Membrane: UL, ultrastructure
Chickens
*Cytoskeleton: ME, metabolism
Intestinal Mucosa: UL, ultrastructure
*Microvilli: UL, ultrastructure
Molecular Weight
CHEMICAL NAME: 0 (Actins); 0 (Carrier Proteins); 0 (villin)

L5 ANSWER 59 OF 59 MEDLINE DUPLICATE 24
ACCESSION NUMBER: 77144287 MEDLINE
DOCUMENT NUMBER: 77144287 PubMed ID: 191636
TITLE: RNA synthesis of vesicular stomatitis virus. VII. Complete

separation of the mRNA's of vesicular stomatitis virus by duplex formation.

AUTHOR: Freeman G J; Rose J K; Clinton G M; Huang A S

SOURCE: JOURNAL OF VIROLOGY, (1977 Mar) 21 (3) 1094-104.
Journal code: KCV; 0113724. ISSN: 0022-538X.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197705
ENTRY DATE: Entered STN: 19900313
Last Updated on STN: 19900313
Entered Medline: 19770527

ABSTRACT:
Full-length virion RNA and complementary mRNA's of vesicular stomatitis virus can be **annealed** to **each other**, digested with RNases, and then separated as five unique duplex RNA molecules on polyacrylamide slab gels. Similar RNA duplexes were detected whether mRNA or virion RNA was the radioactive component and whether the mRNA was synthesized in vitro or in vivo. The sharp banding pattern of these RNA molecules was dependent on treatment with RNase T2, suggesting that removal of poly(A) is necessary. Identification of the coding region contained in each RNA duplex was based on their previous identification as single-stranded mRNA on formamide-containing, polyacrylamide gels. Because the two smallest mRNA'S had not been previously separated, their identification was based on their in vitro transcriptional gene order. In the order of increasing mobilities on the slab gels, the RNA duplexes are identified as the hybrid of the region of the genome RNA hybridized to the complementary mRNA coding for the large protein, the glycoprotein, the nucleocapsid protein, the core-associated NS protein, and the matrix protein (L,G,N,NS, and M). Several lines of evidence support the presence of undegraded complete mRNA, excluding poly(A), in these RNA duplexes. Also, the two smallest mRNA's, separated by duplex formation, were denatured, and their individual **oligonucleotide** fingerprints were determined. From chemical length determinations, the molecular weights of the mRNA, minus poly(A), are 2.78 X 10(5) and 2.5 X 10(5), respectively, for the mRNA's of the NS and M proteins.

CONTROLLED TERM: Check Tags: Support, U.S. Gov't, P.H.S.
Cell Line
Molecular Weight
Nucleic Acid Denaturation
Nucleic Acid Hybridization
Oligonucleotides: AN, analysis
*RNA, Messenger: AN, analysis
RNA, Messenger: BI, biosynthesis
*RNA, Viral: AN, analysis
RNA, Viral: BI, biosynthesis
Ribonucleases: ME, metabolism
*Vesicular Stomatitis-Indiana Virus: AN, analysis
Vesicular Stomatitis-Indiana Virus: ME, metabolism

CHEMICAL NAME: 0 (**Oligonucleotides**); 0 (RNA, Messenger); 0 (RNA, Viral); EC 3.1.- (Ribonucleases)